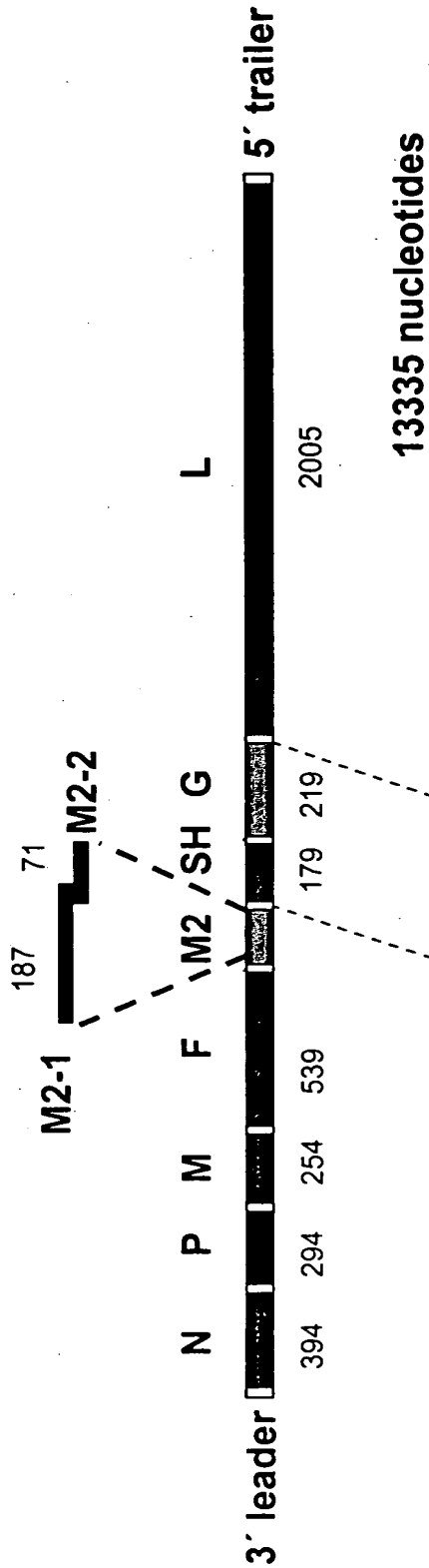


HMPV 83



RSV A2

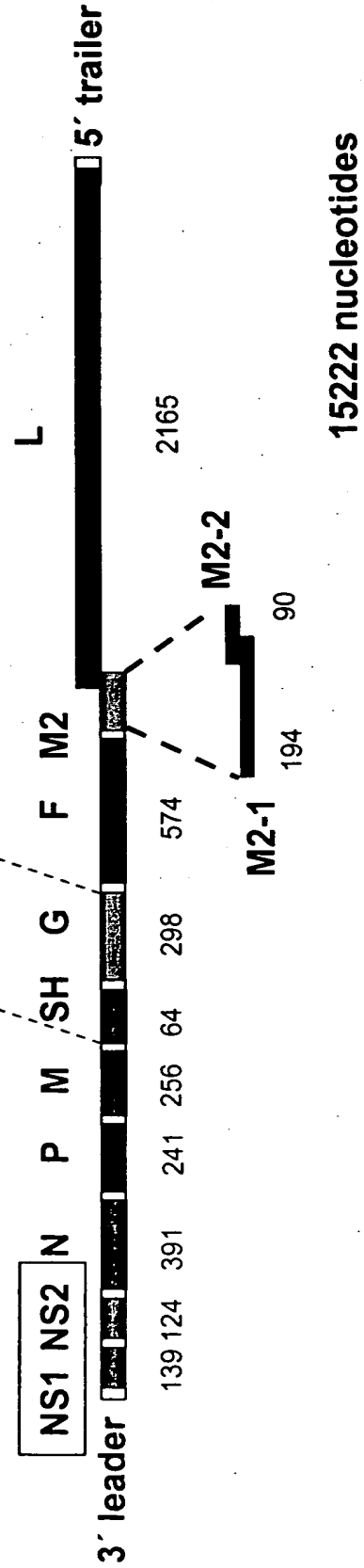


Fig. 1

Fig. 2

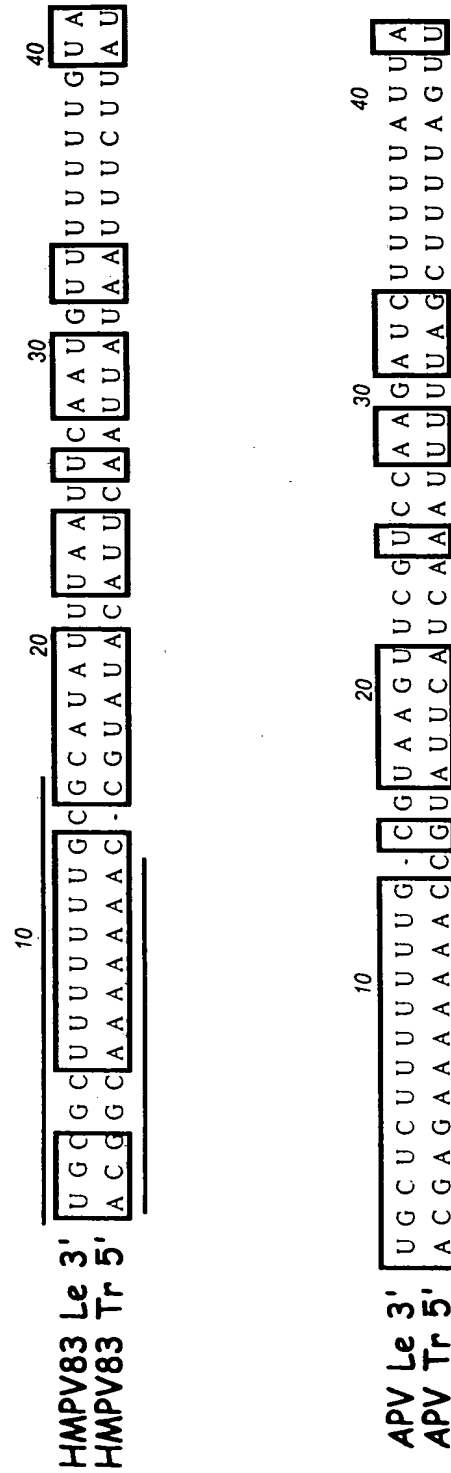


Fig. 3

Examples of differences between HMPV 83 and HMPV 00-1

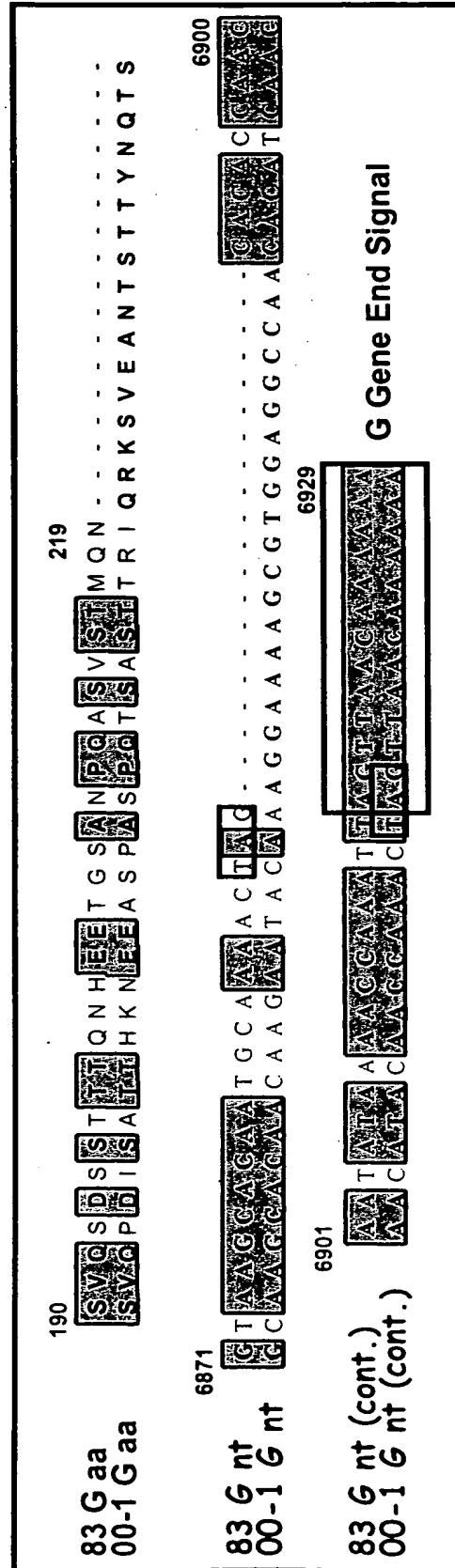


Fig. 4

Amino acid identity between HMPV83 and other Pneumoviruses for the indicated proteins

	N	P	M	F	M 2-1	M 2-2	G	SH	L
HMPV 00-1	99	95	99	98	98	96	70	85	99
HMPV 97-82	95	85	97	94	ND	ND	ND	ND	ND
APV A	70	58	77	68	73	25	12	20	64
APV B	69	53	76	67	71	27	ND	20	ND
APV C	88	68	87	81	83	56	ND	ND	ND
HRSV A2	41	31	38	36	36	12	15	6	46
HRSV B	41	31	37	35	35	8	15	6	46
BRSV	41	31	37	37	35	14	19	10	46
PVM	45	28	38	40	36	12	ND	8	ND

ND: Comparison not done, usually because sequence was unavailable

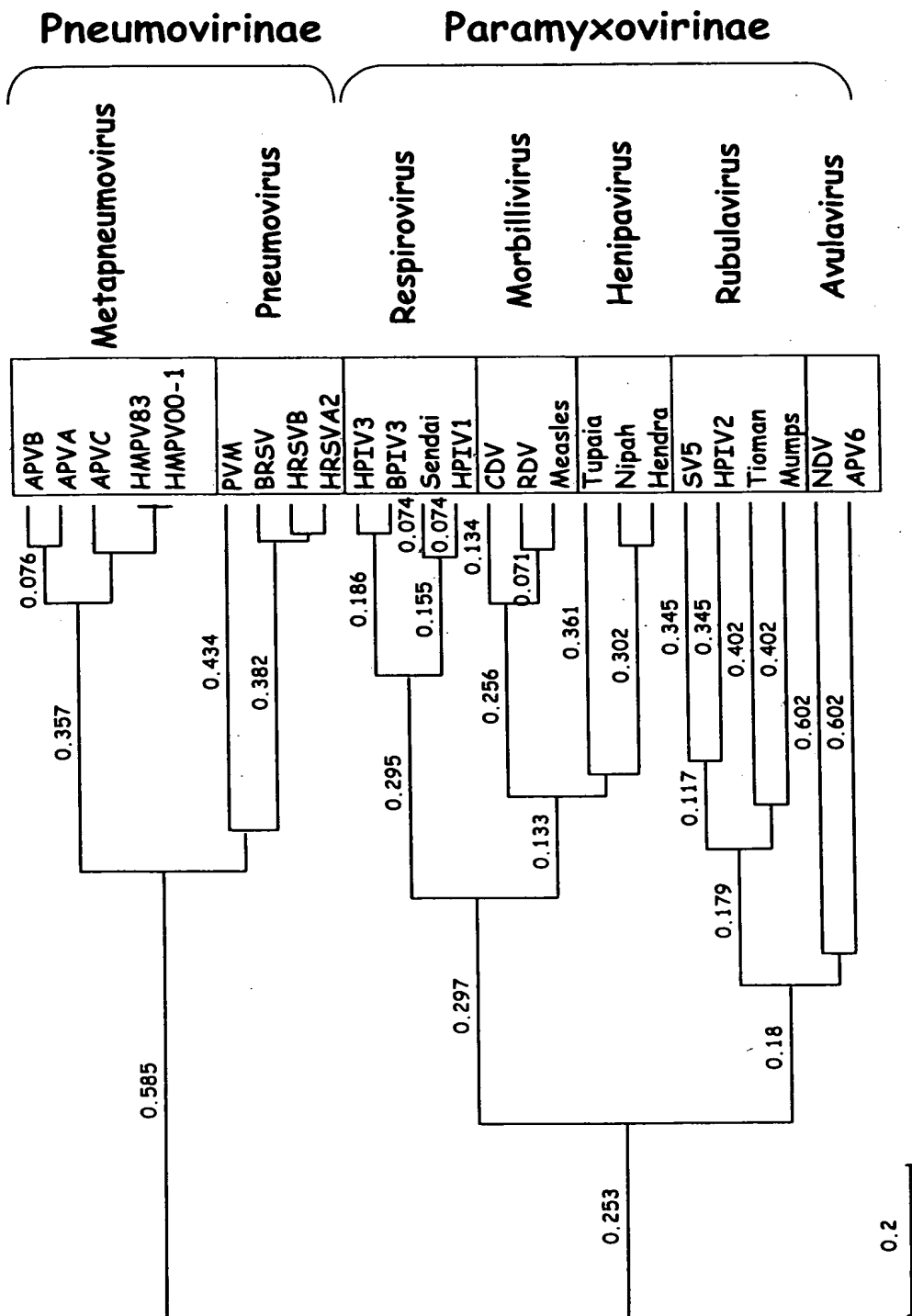


Fig. 6

HMPV 83 13335 bases

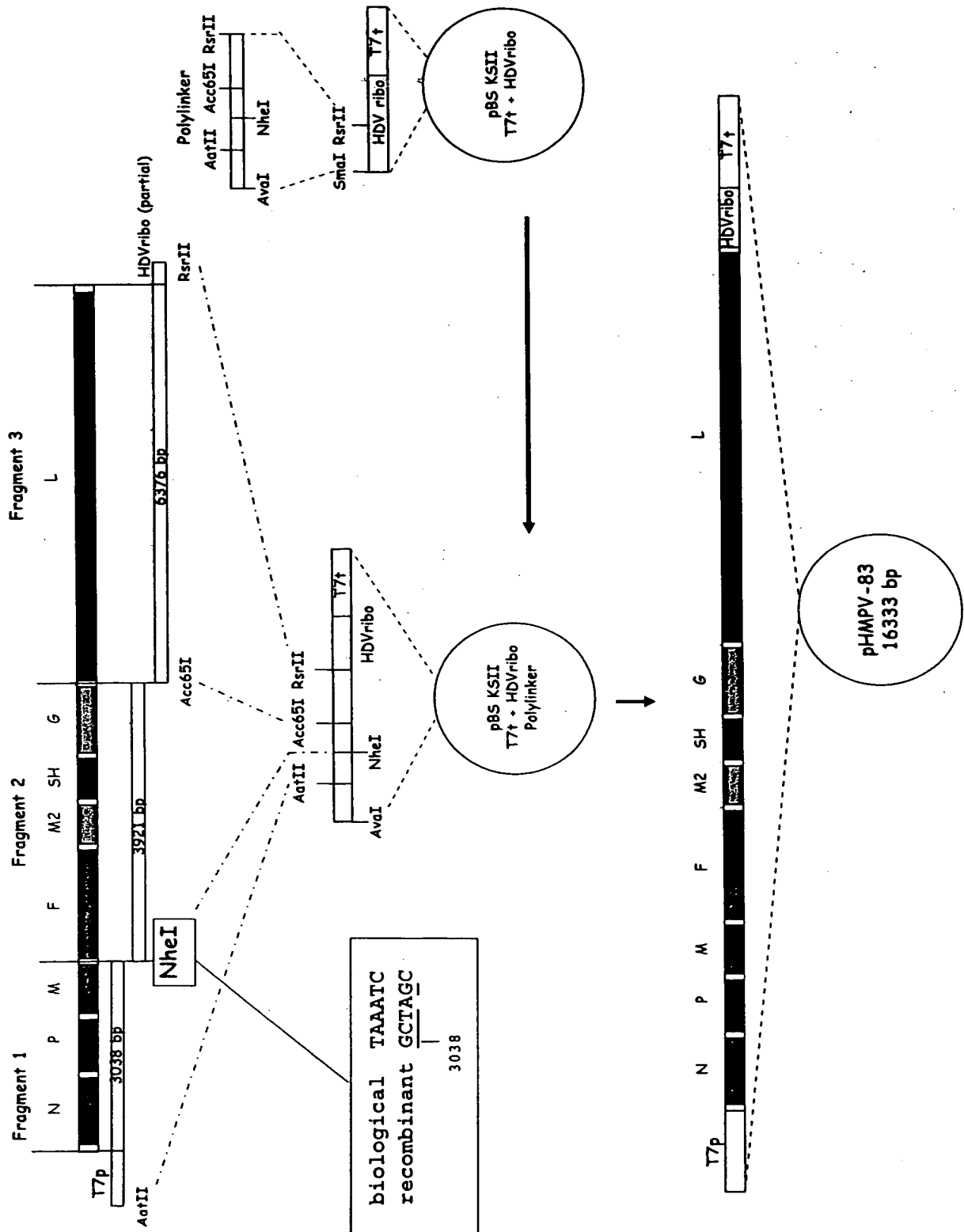


Fig. 7

Gene Start Signal

	1	5	10	15
N	tacaaaaaacat	GGGACAAAGTGAAA	ATGtctcttc	
P	taattaaaaaagt	GGGACAAAGTCAAA	ATGtcattcc	
M	aaaaataaaaaat	GGGACAAAGTGAAA	ATGgagtcct	
F	atcaatcaagaac	GGGACAAATAAAA	ATGtcttggg	
M2	taaaataaaaattt	GGGACAAATCATA	ATGtctcgca	
SH	aacacatcagagt	GGGATAAGTGACA	ATGataacat	
G	aaaacaaaaatat	GGGACAAAGTAGTT	ATGgaggtga	
L	aaacagcatccaa	GAGACAAATAGCA	ATGgatcctc	

CONSENSUS ...at **GGGACAAAGTGAAA** **ATGtc...**
gc A T A AGTT ga
ta C C at

Gene End Signal

	1	5	10
N	ttatg	AGTAATTAAAAAA	gt
P	tatgt	AGTTTAATAAAAA	taaaaaat
M	atttt	AGTTATATAAAAA	tcaagttagaat a
F	cagtt	AGTTAATTAAAAA	taaaataaaaatt t
M2	actta	AGTTAGTAAAAA	cacatcagagt
SH	agttt	AGTTATTTTAAAA	tatttgagaata g
G	aaatt	AGTTAACAAAAAA	tacgagatagct c
L	atgat	AGTTAATTAAAAA	ttaaaaaattaaaa a

CONSENSUS ...tt **AGTTAATTAAAAA** ta...
ag ATTAAT . cc
ga GC gt

Fig. 8

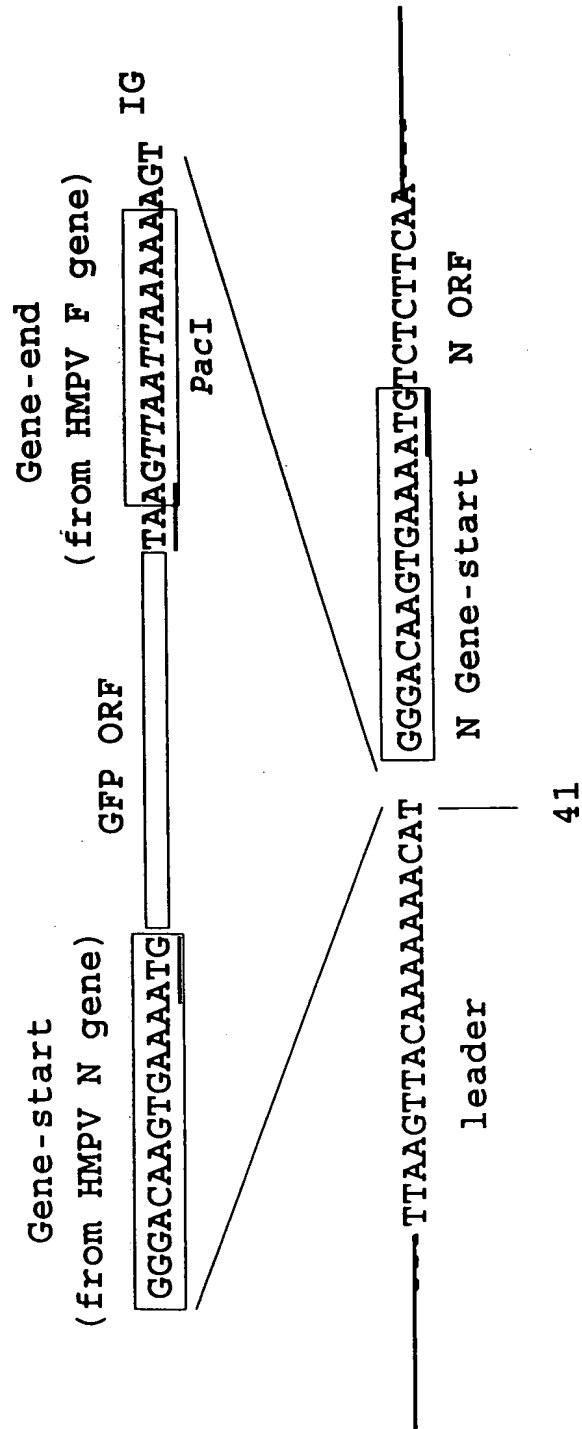


Fig. 9

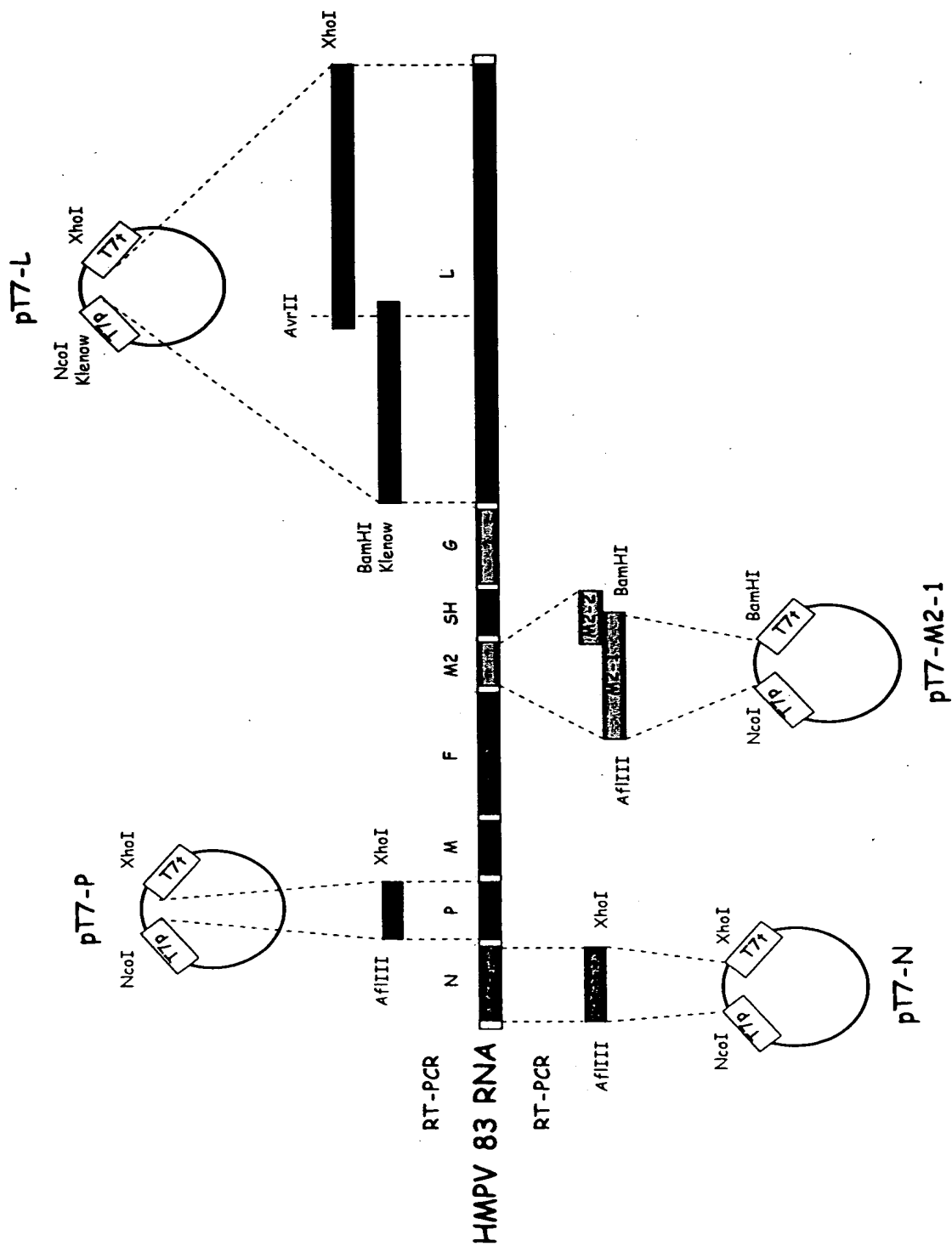


Fig. 10

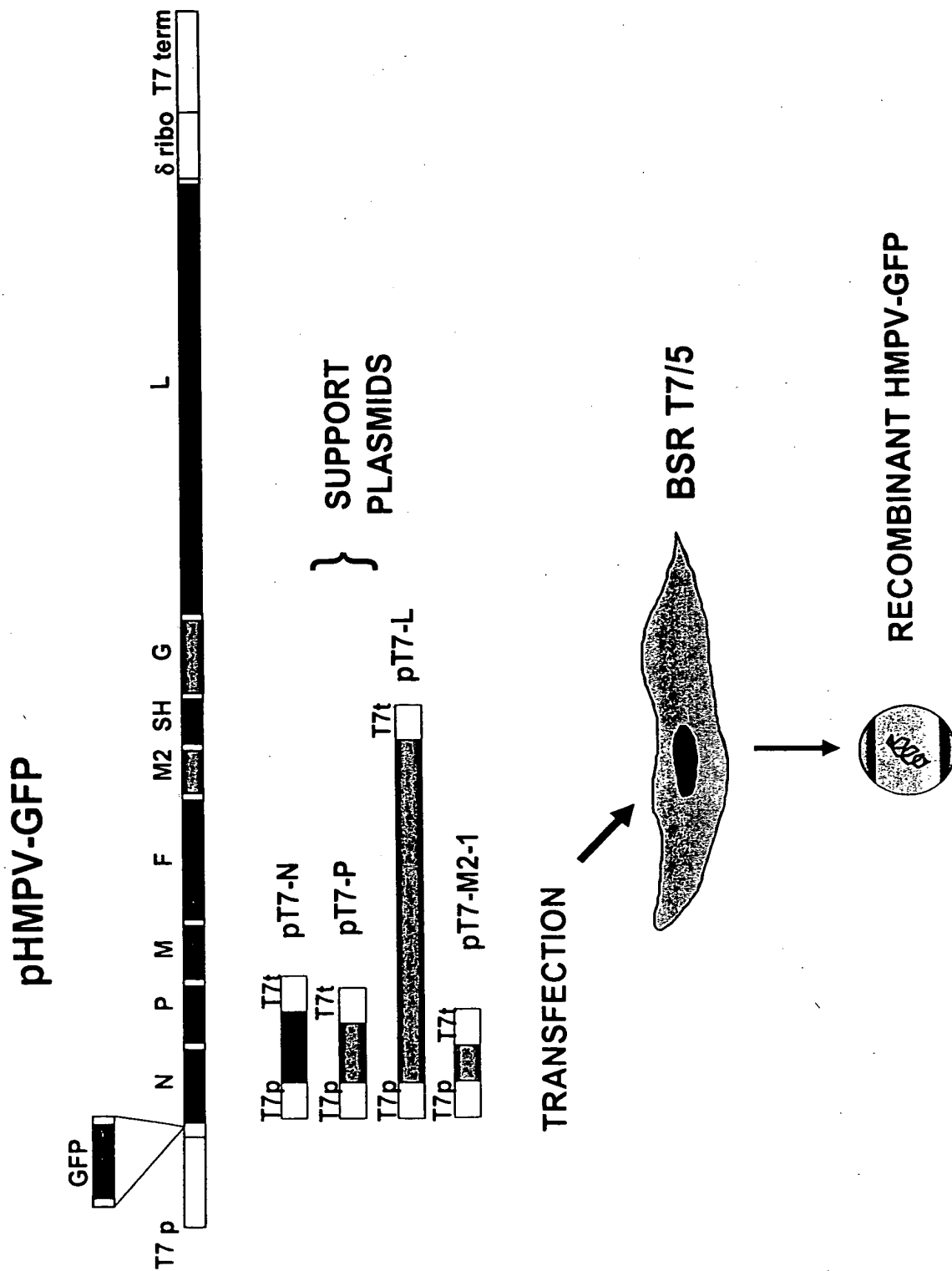


Fig. 11

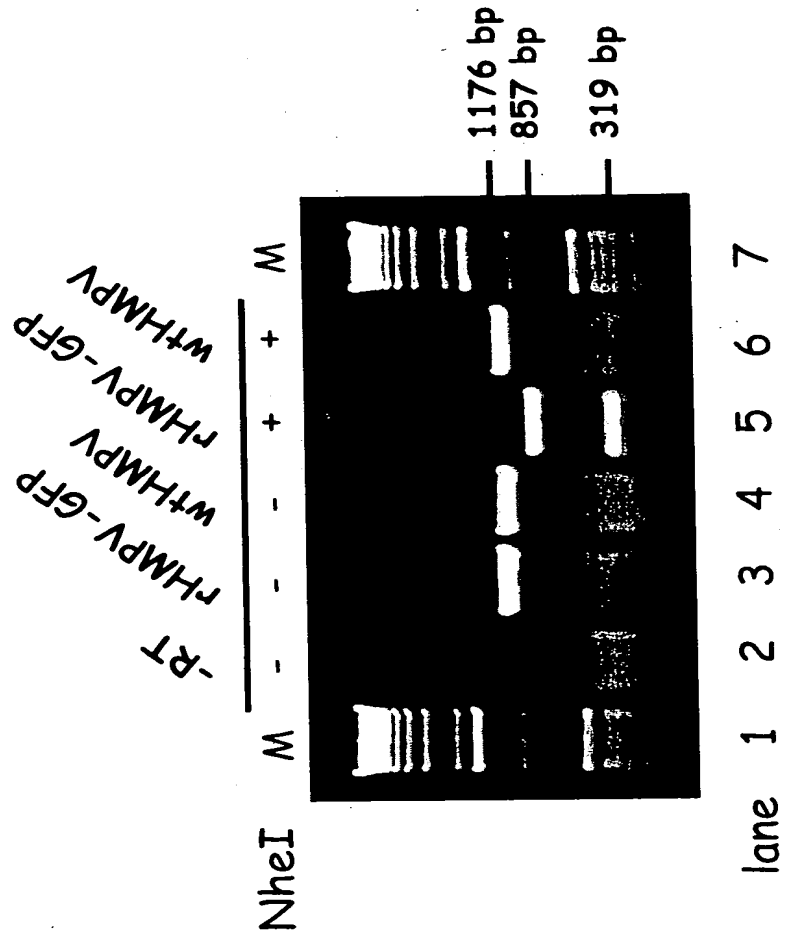


Fig. 12A

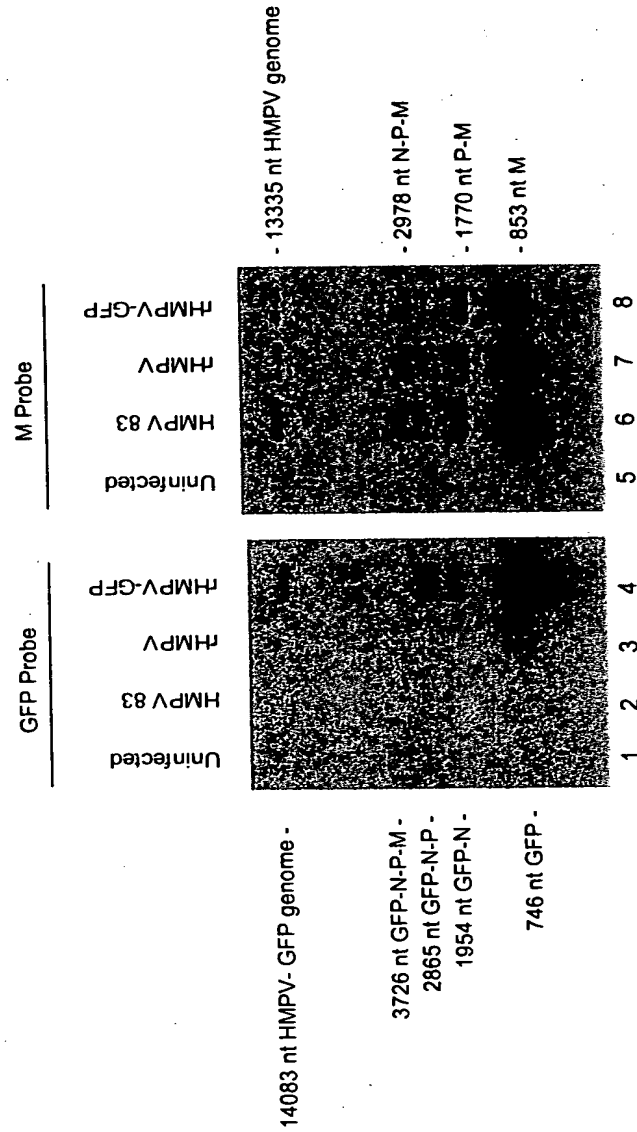


Fig. 12B

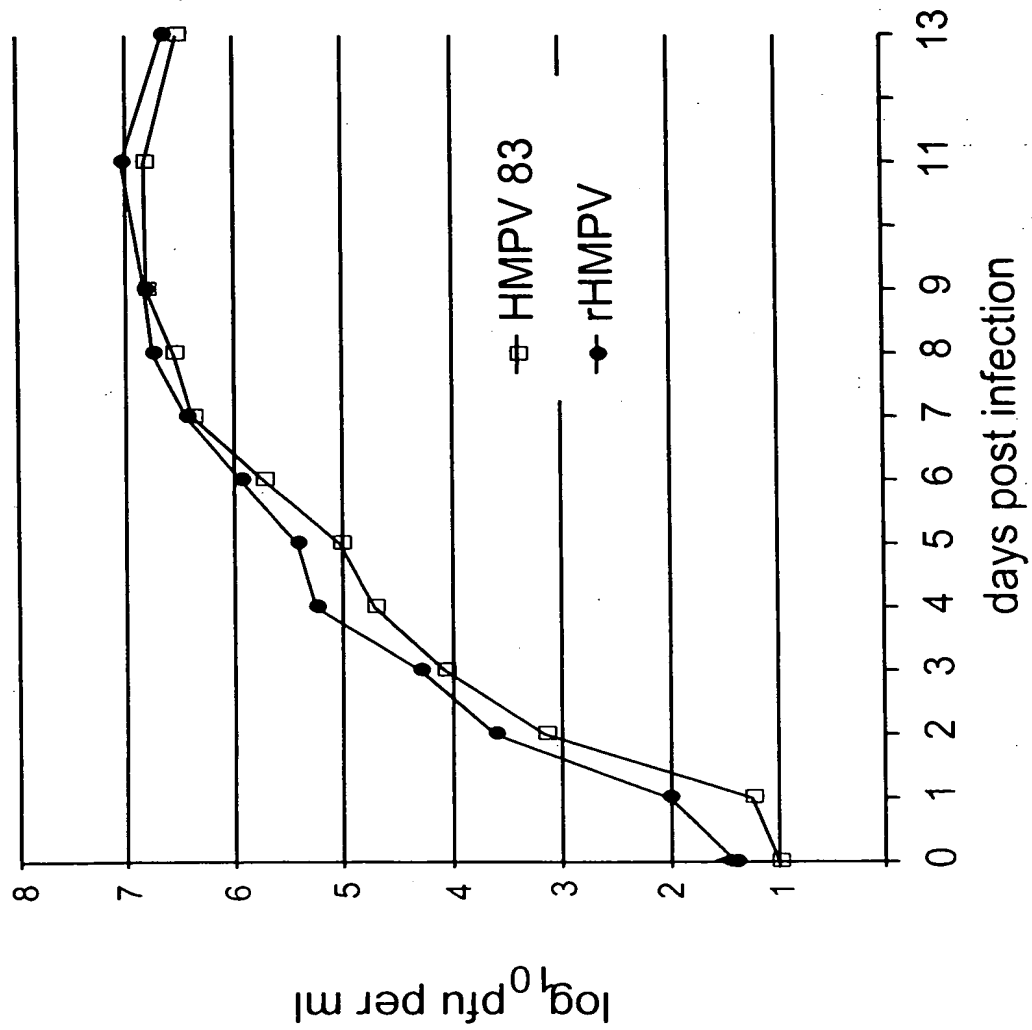


Fig. 13

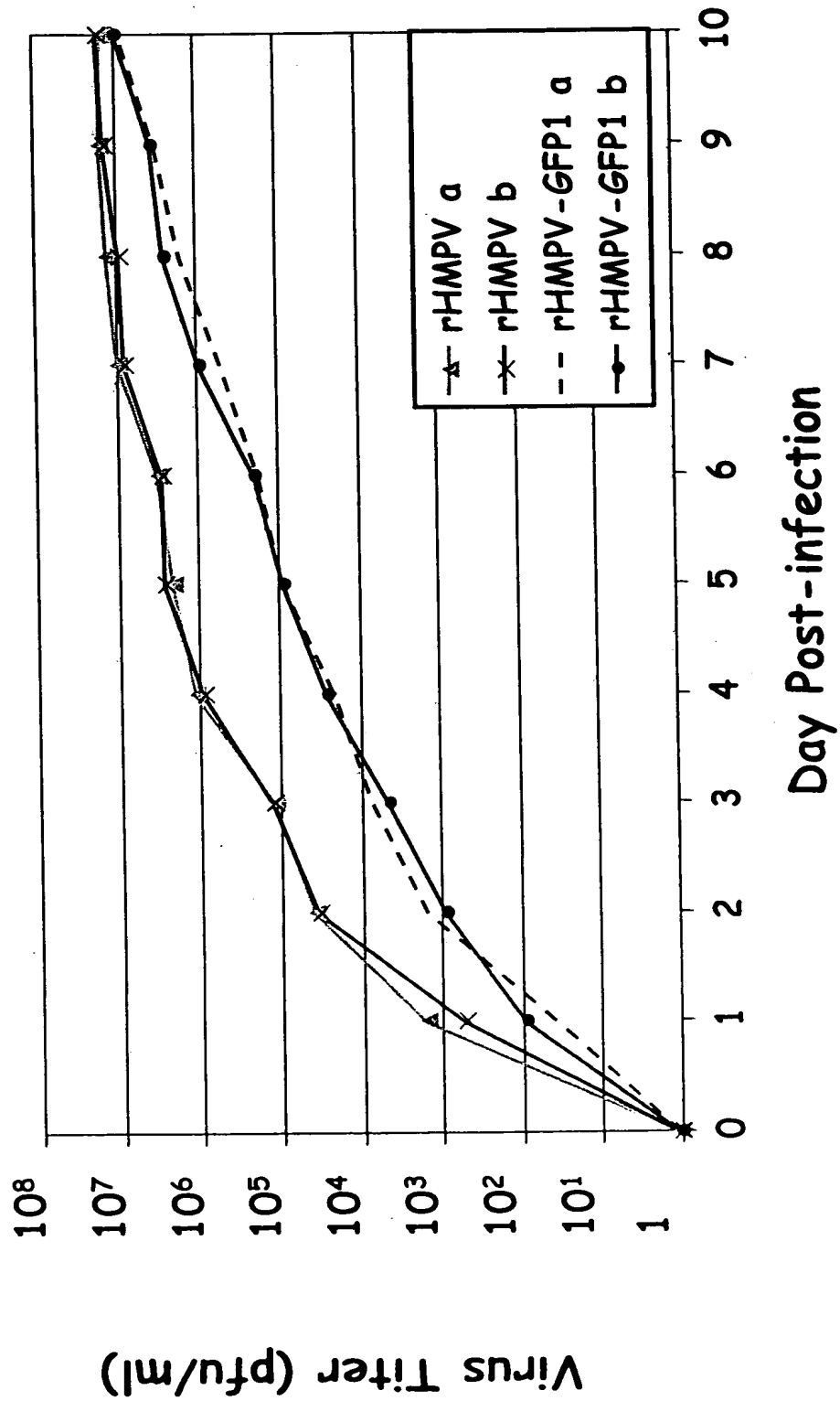


Fig. 14

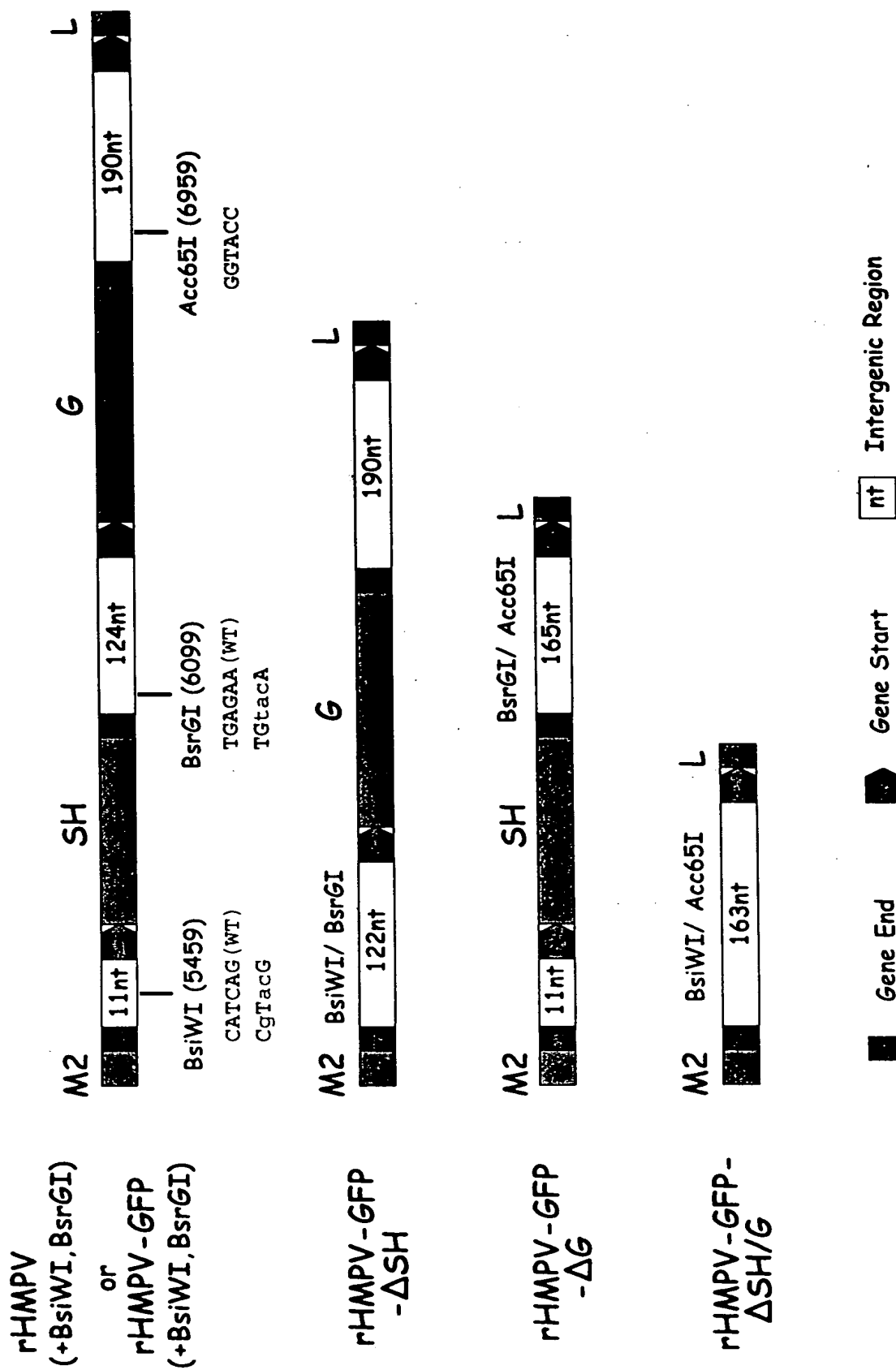


Fig. 15

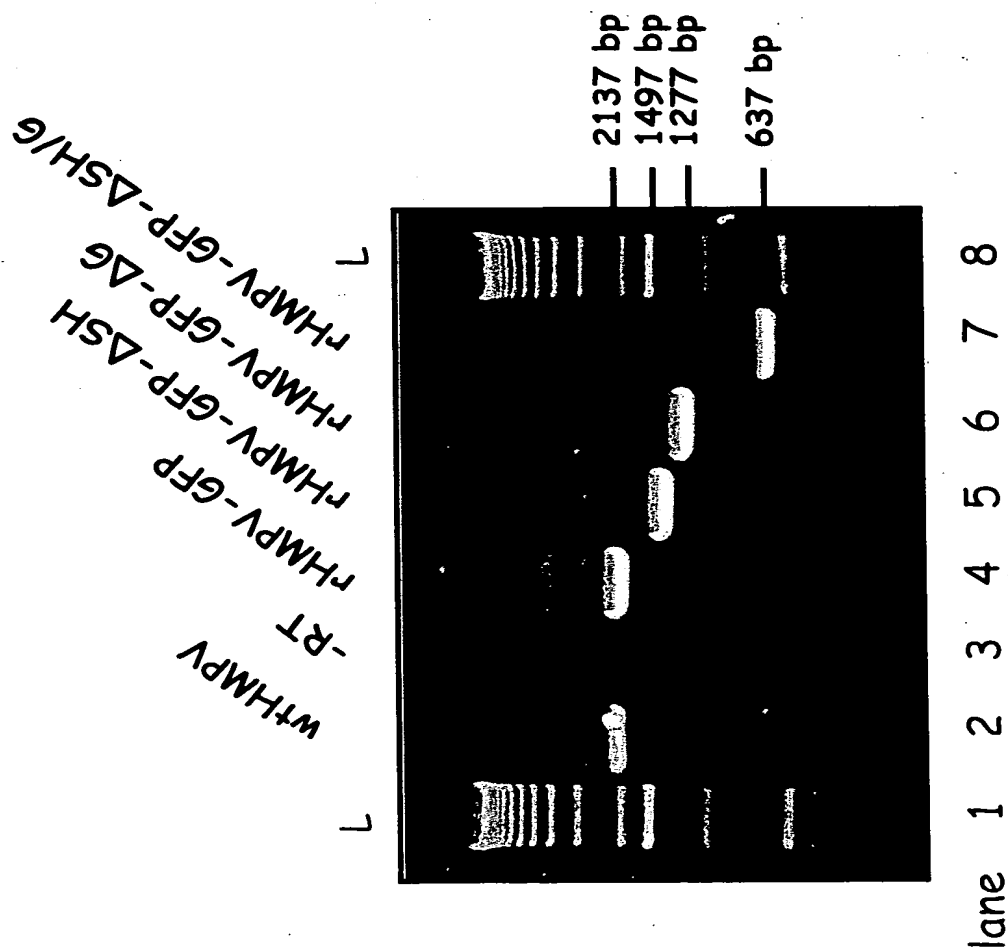


Fig. 16

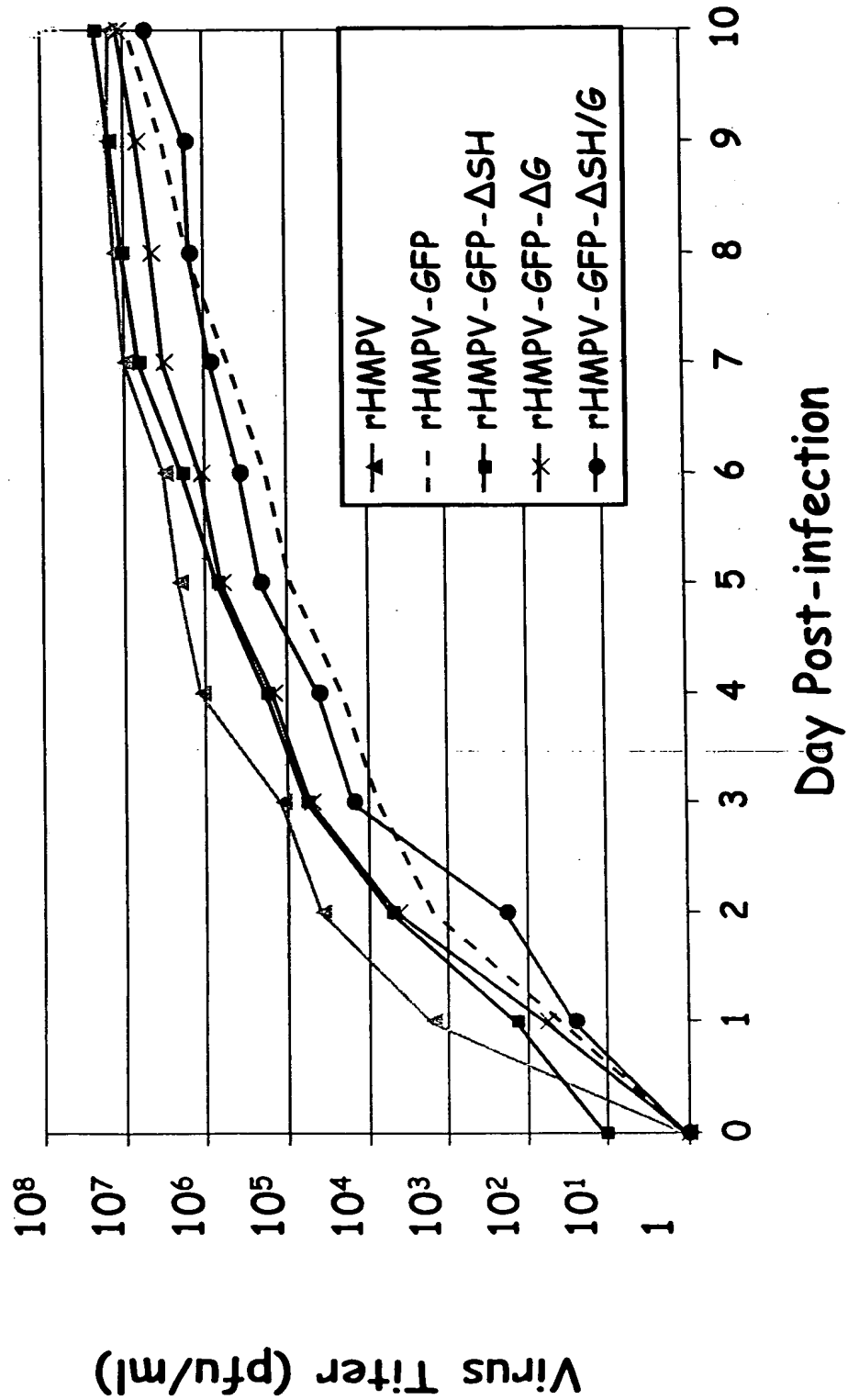


Fig. 17A

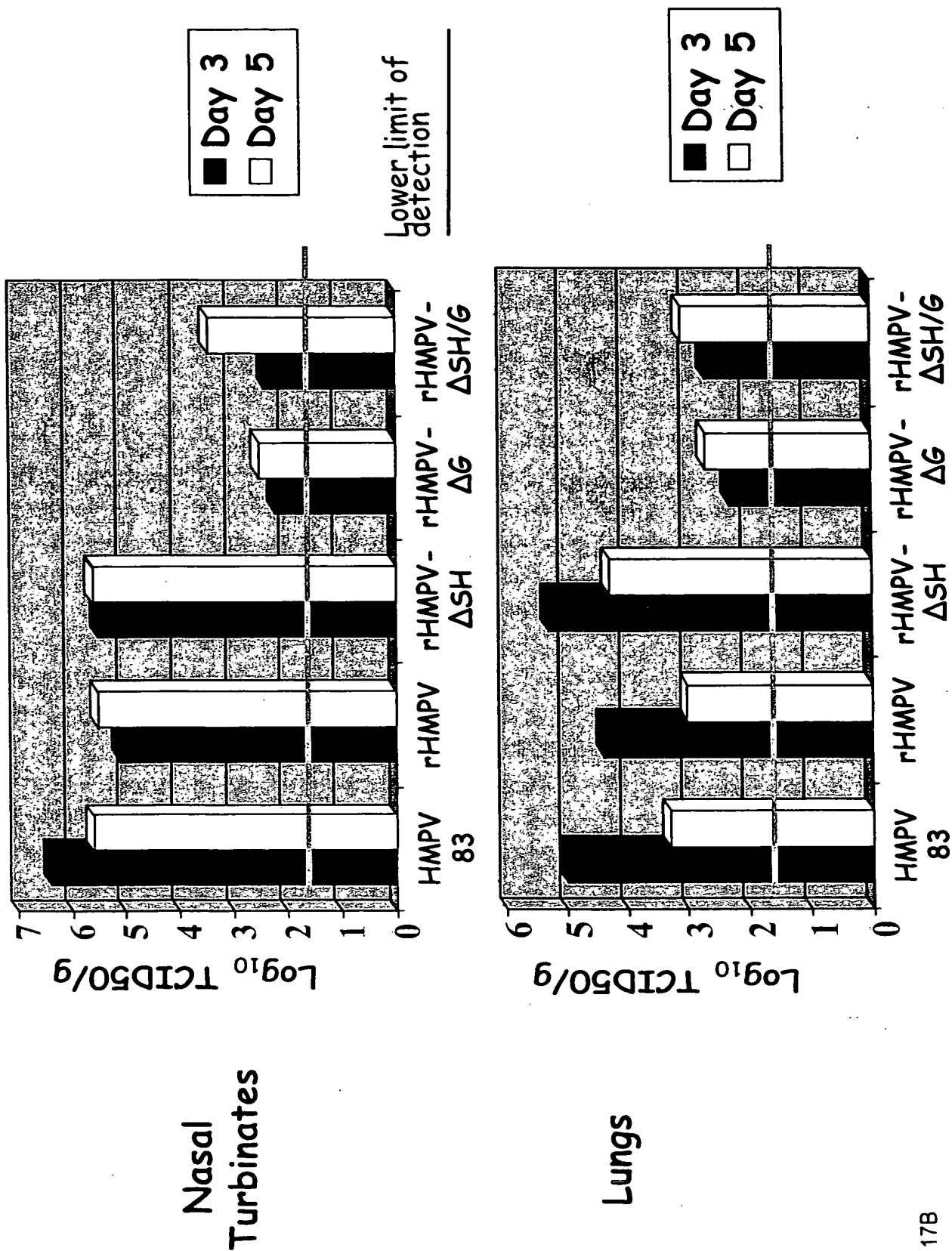


Fig. 17B

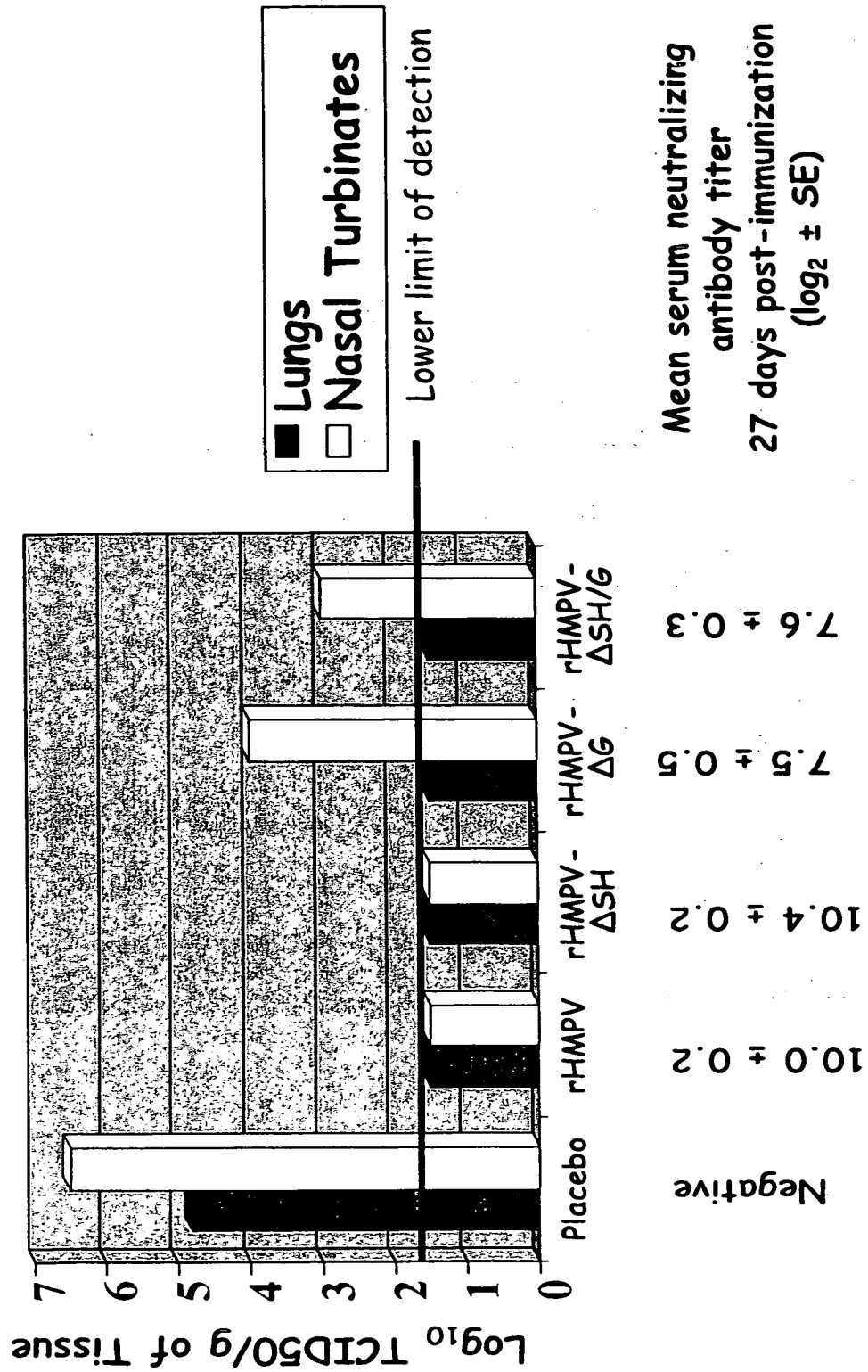


Fig. 17C

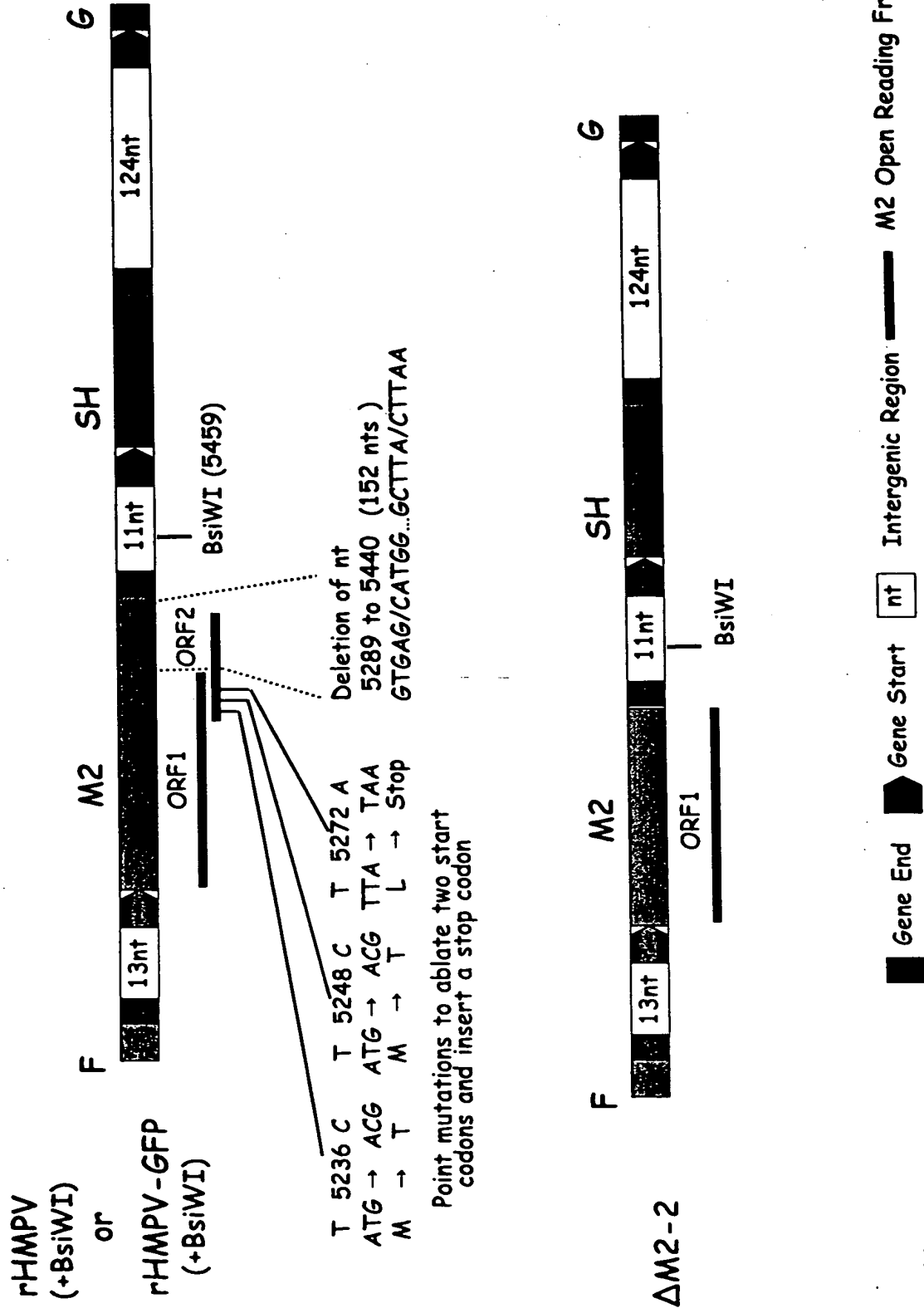


Fig. 18A

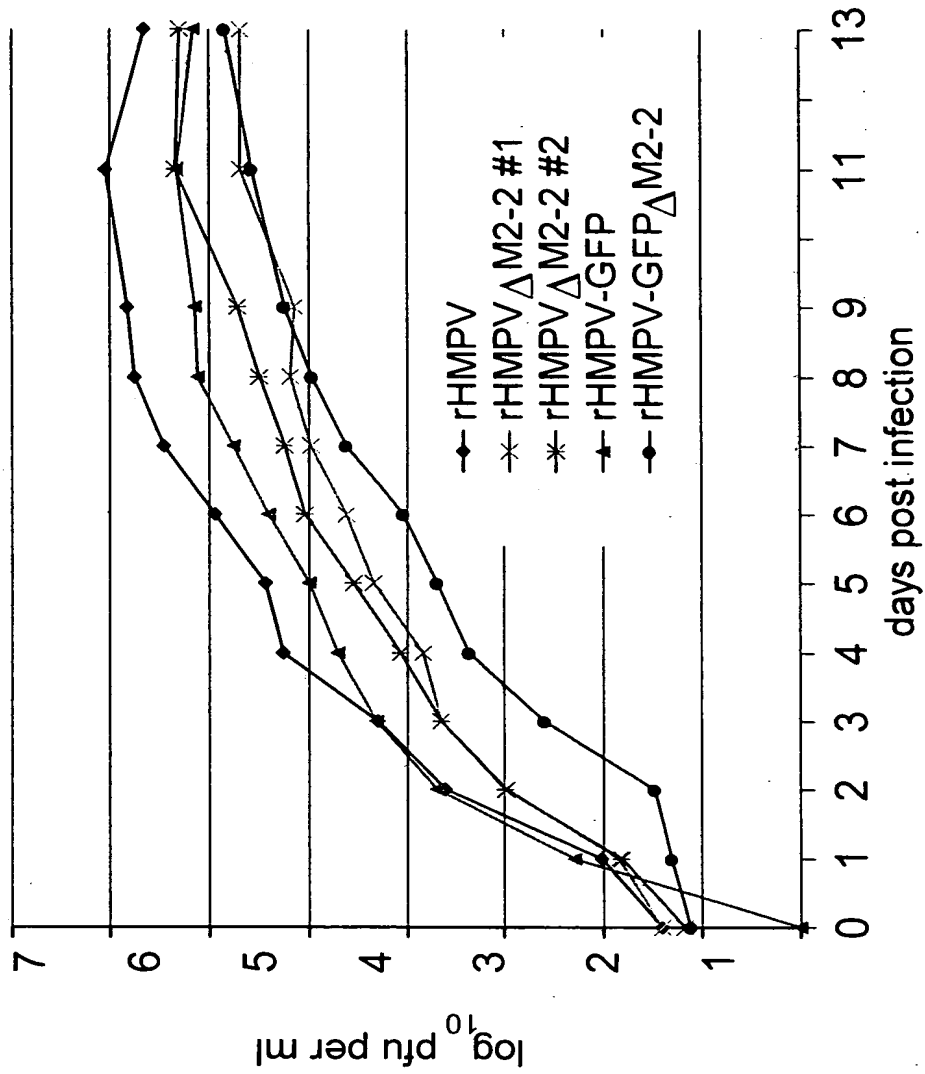


Fig. 18B

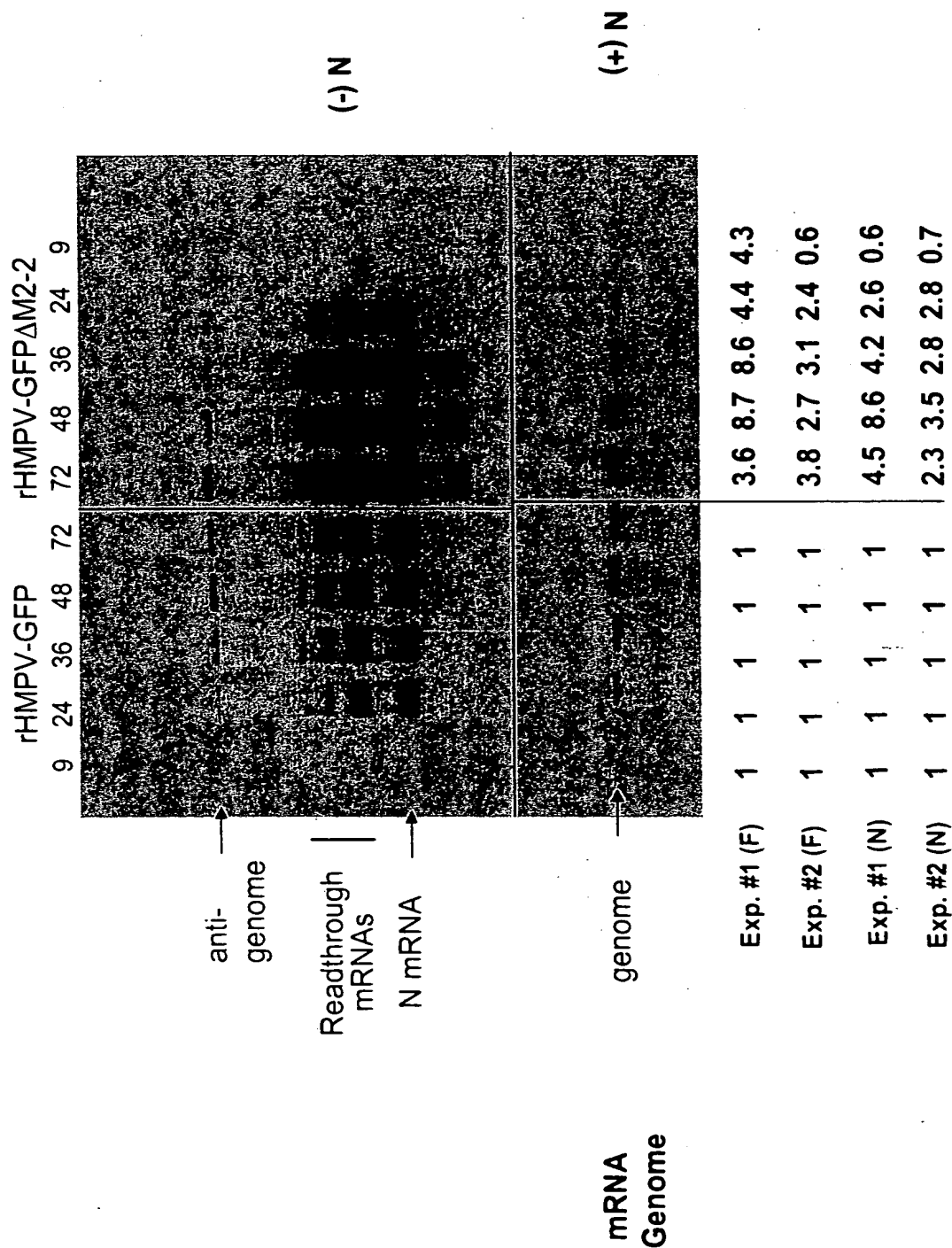


Fig. 18C

	C	X7	C	X5	C	X3	H
HMPV-GFP M2 C7S	M	S	R	K	A	P	C
HMPV-GFP M2 Y9S	M	S	R	K	A	P	C
HMPV-GFP M2 C15S	M	S	R	K	A	P	C
HMPV-GFP M2 N16S	M	S	R	K	A	P	C
HMPV-GFP M2 H25S	M	S	R	K	A	P	C

C	K	Y	E	V	R	G	K	C	N	R	G	S	E	C	K	F	N	H	N
S	K	Y	E	V	R	G	K	C	N	R	G	S	E	C	K	F	N	H	N
C	K	Y	S	E	V	R	G	K	C	N	R	G	S	E	C	K	F	N	H
C	K	Y	E	V	R	G	K	S	C	N	R	G	S	E	C	K	F	N	H
C	K	Y	E	V	R	G	K	C	N	R	G	S	E	C	K	F	N	H	N
C	K	Y	E	V	R	G	K	C	N	R	G	S	E	C	K	F	N	H	N
C	K	Y	E	V	R	G	K	C	N	R	G	S	E	C	K	F	N	H	N

Fig. 19

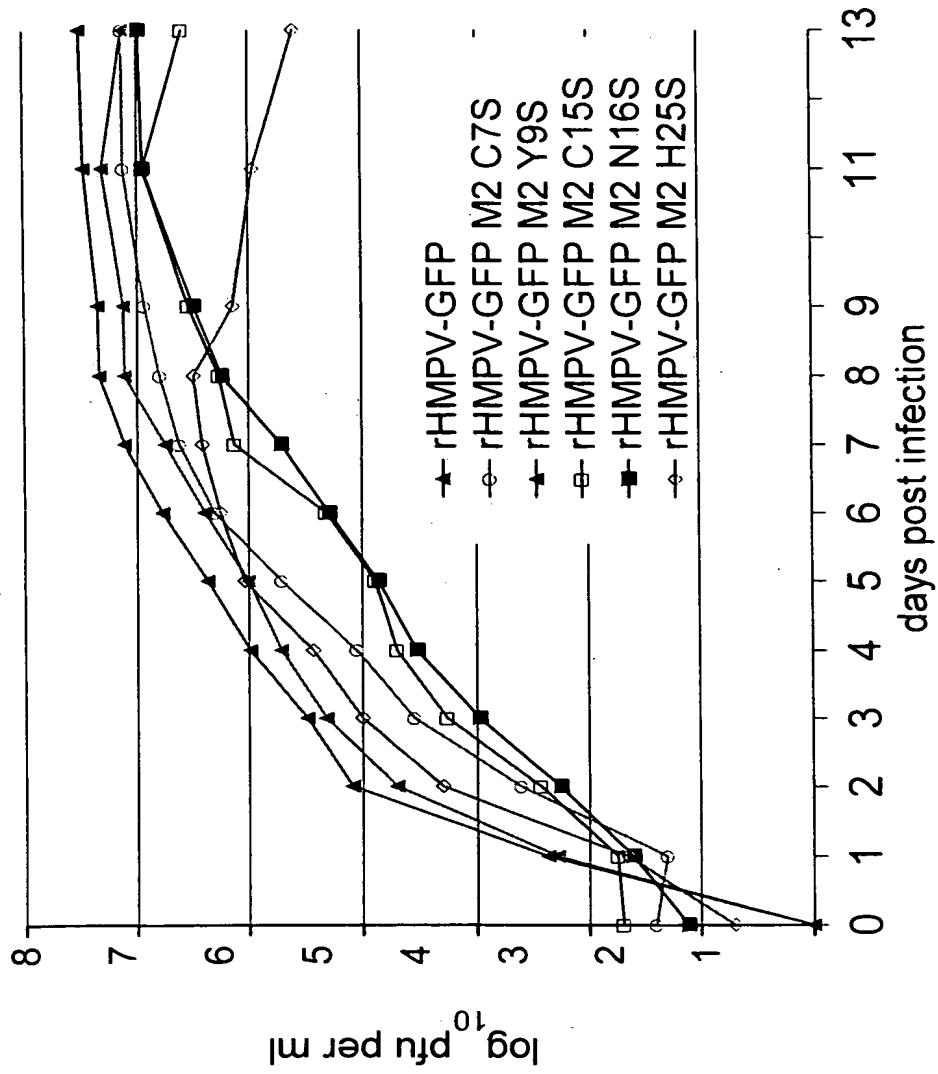


Fig. 20

	4711	GGGACAAATCATAATG	4775
HMPV		TCT CGC AAG GCT CCA TGC AAA TAT GAA GTG CGG GGC AAA TGC AAC AGA	
rHMPV-GFP ΔM2-1		tag M S R K A P C K Y E V R G K C N R	
HMPV		* tag	
rHMPV-GFP ΔM2-1		* N K	

Fig. 21

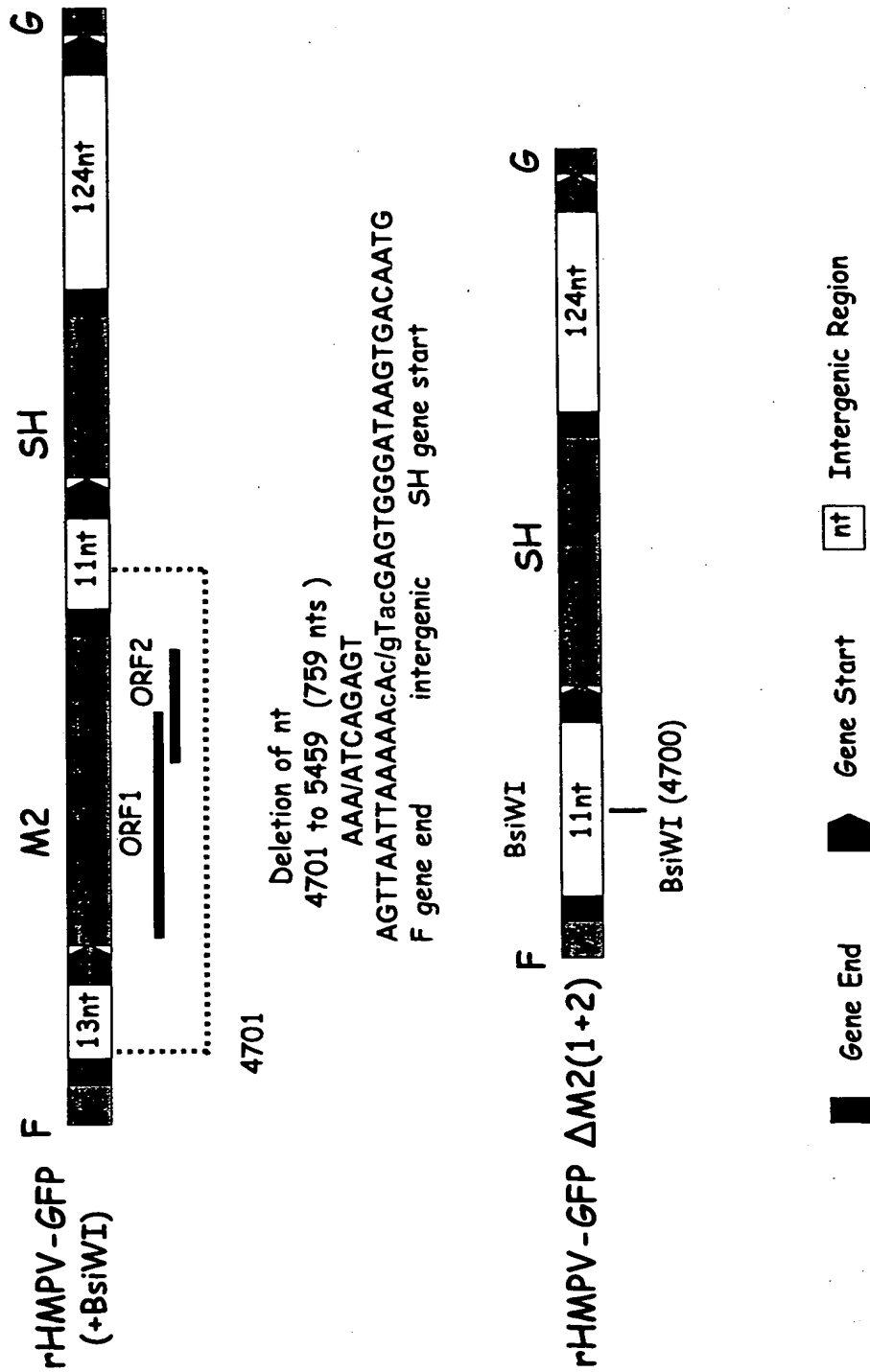


Fig. 22A

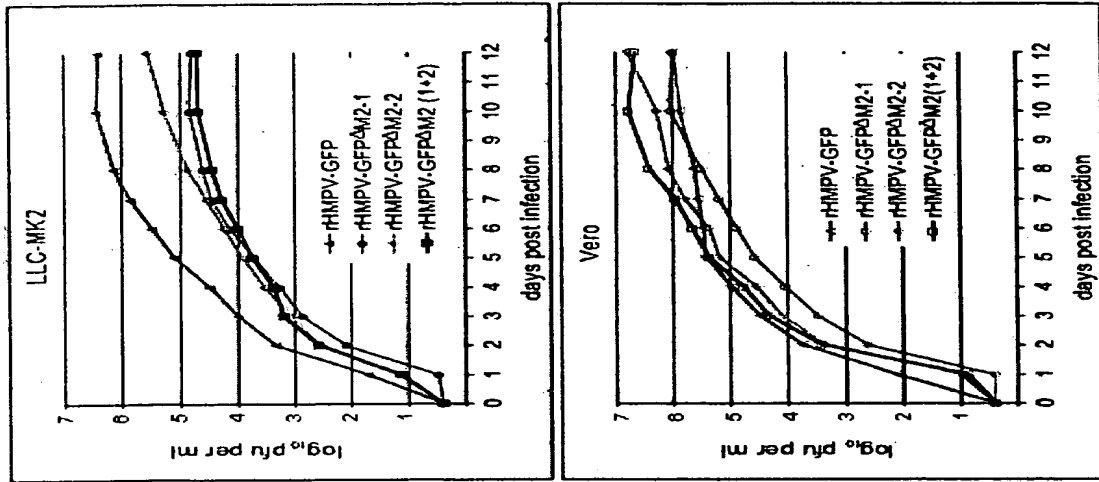


Fig. 22B

Reduction of virus yield in presence of exogenous interferon (IFN) type I

Virus	MOI	Fold reduction of virus yield		
		10 U IFN	100 U IFN	1000 U IFN
rHMPV-GFP	1.0	5	160	1680
rHMPV-GFP Δ M2(1+2)	1.0	19	1130	no virus
rHMPV-GFP Δ M2-2	1.0	13	250	no virus
RSV-GFP	0.01	4	17	90

Fig. 22C

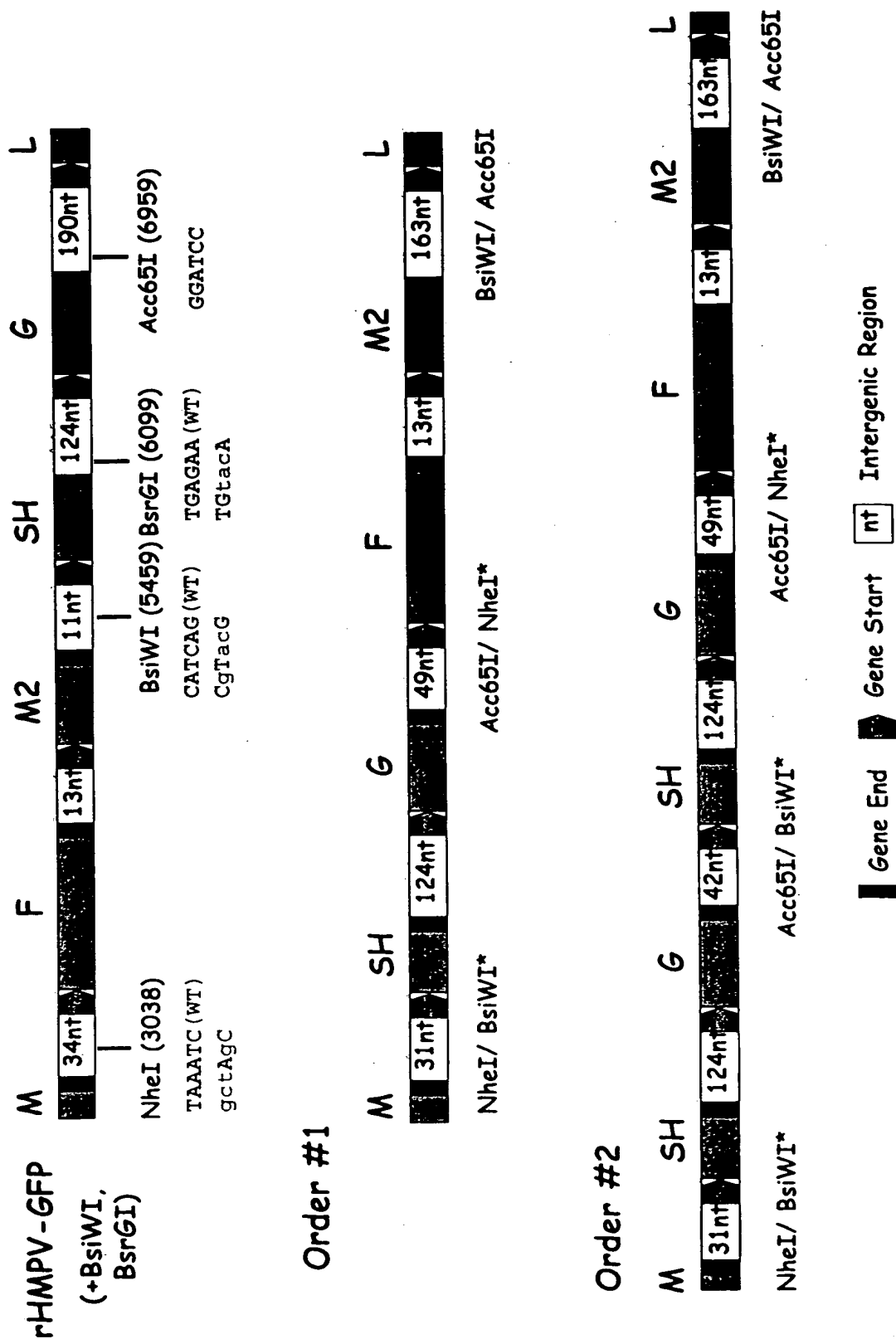


Fig. 23A

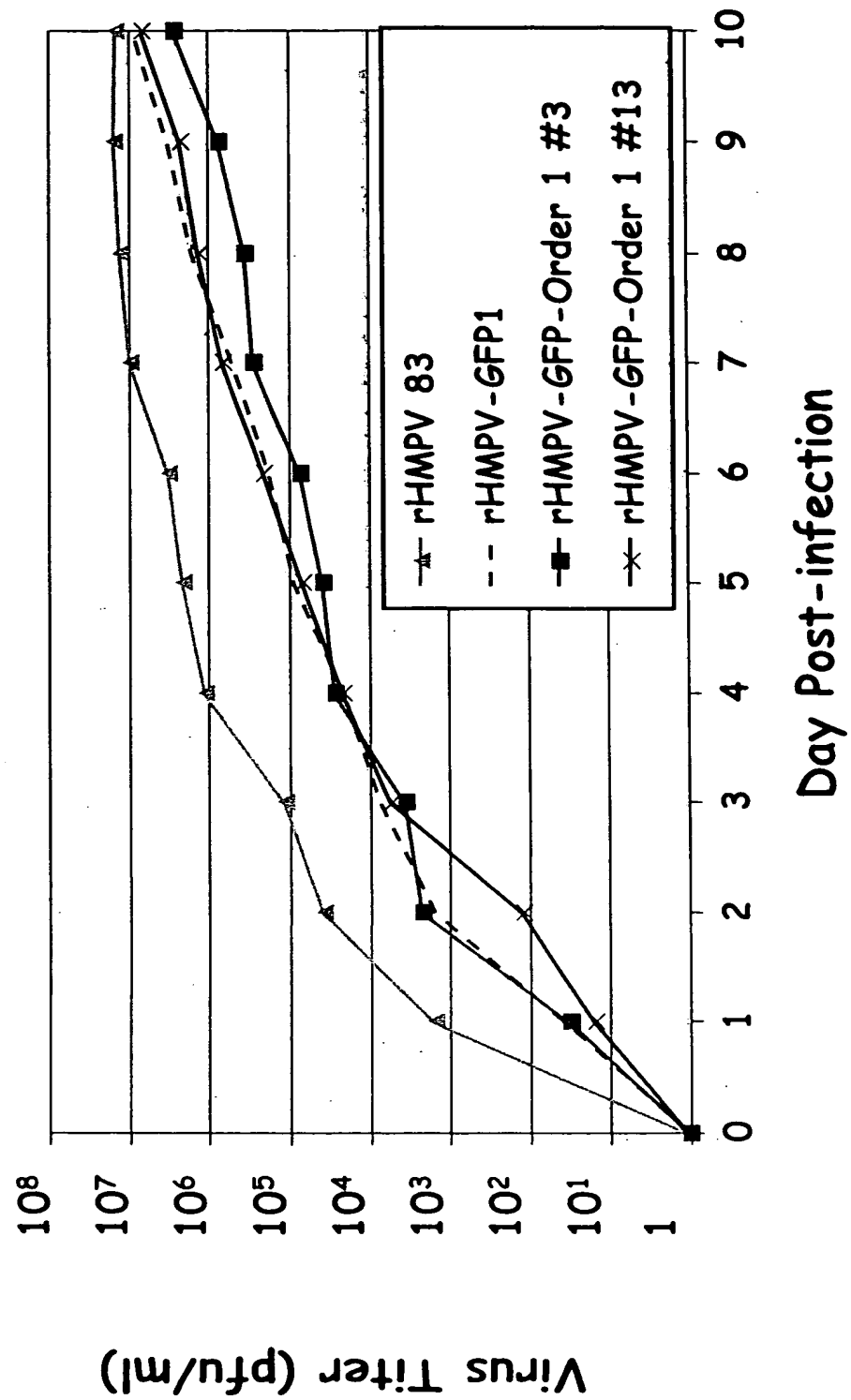


Fig. 23B

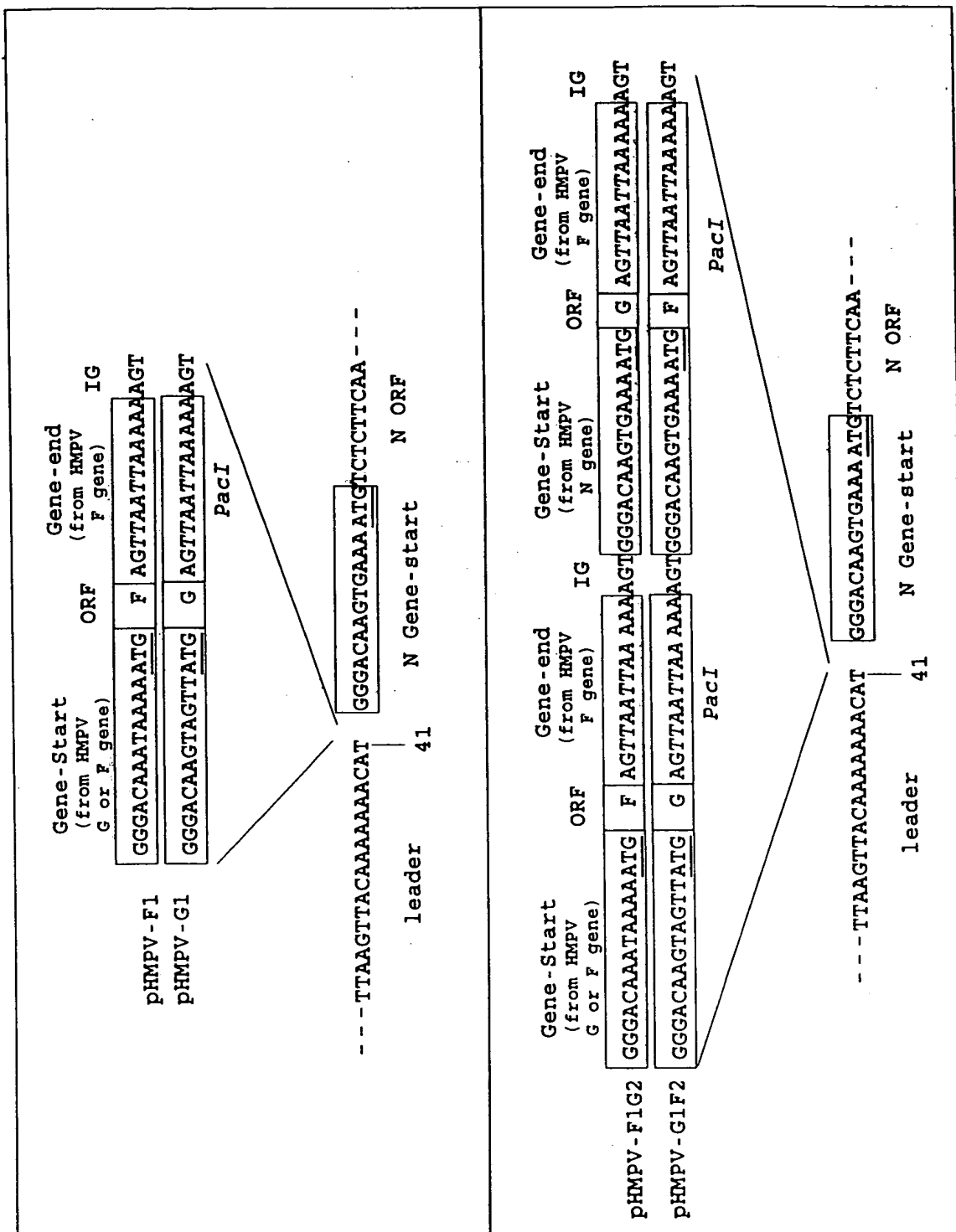


Fig. 24A

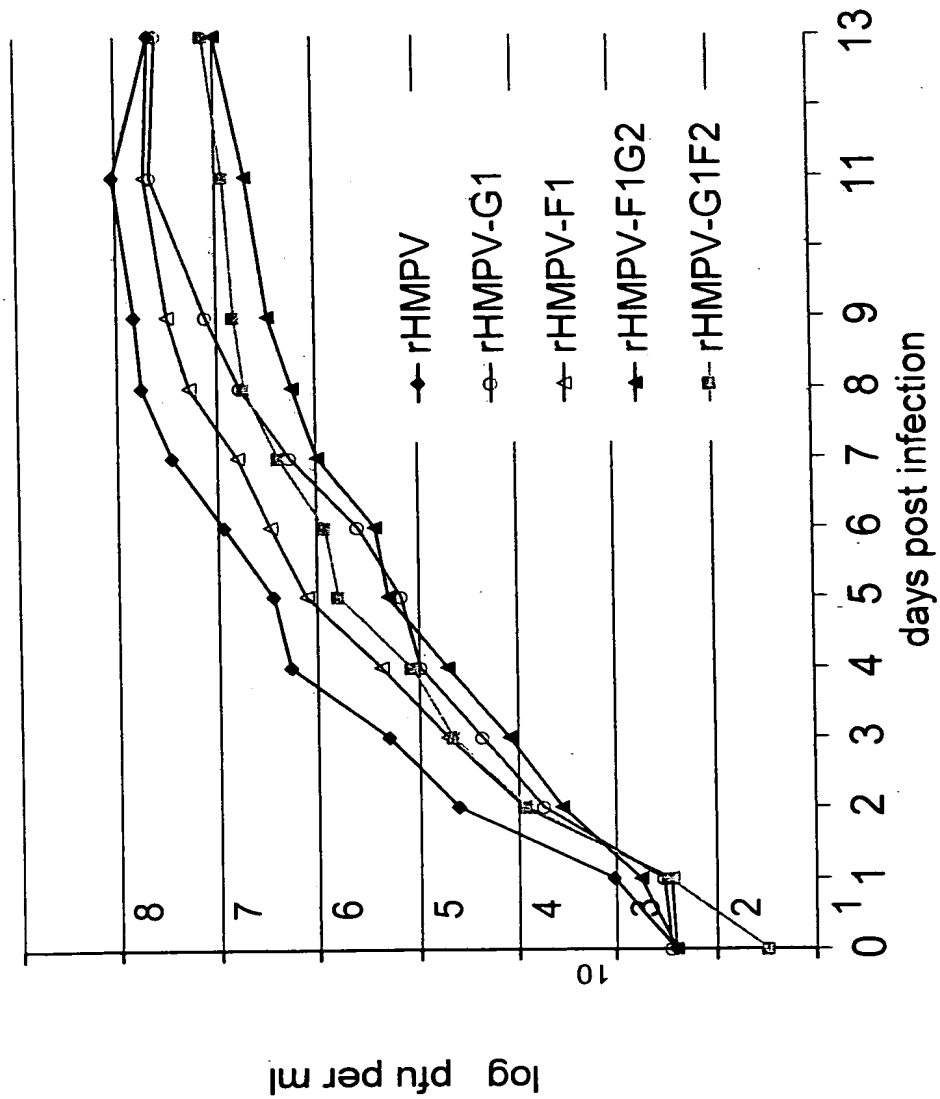


Fig. 24B

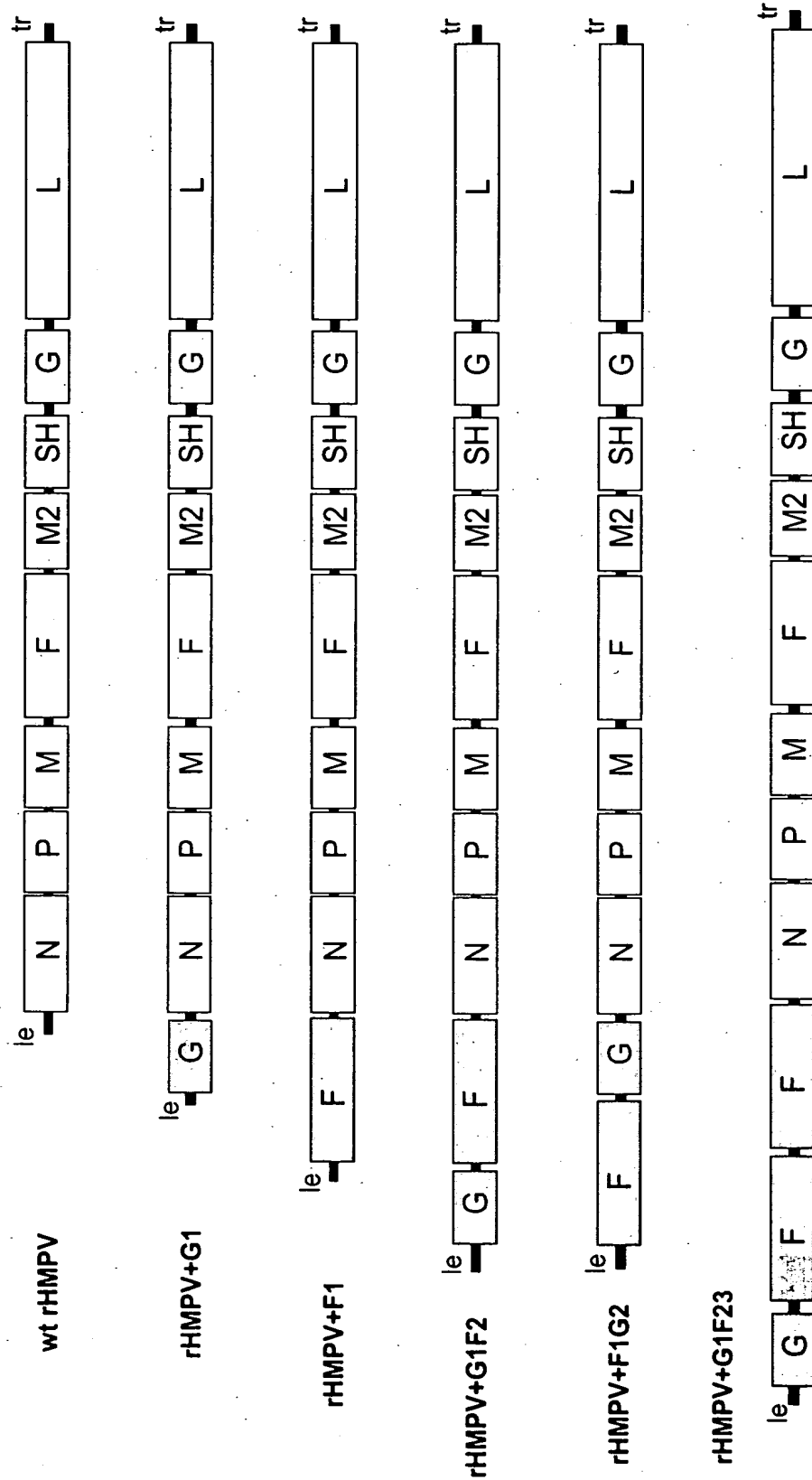


Fig. 25A

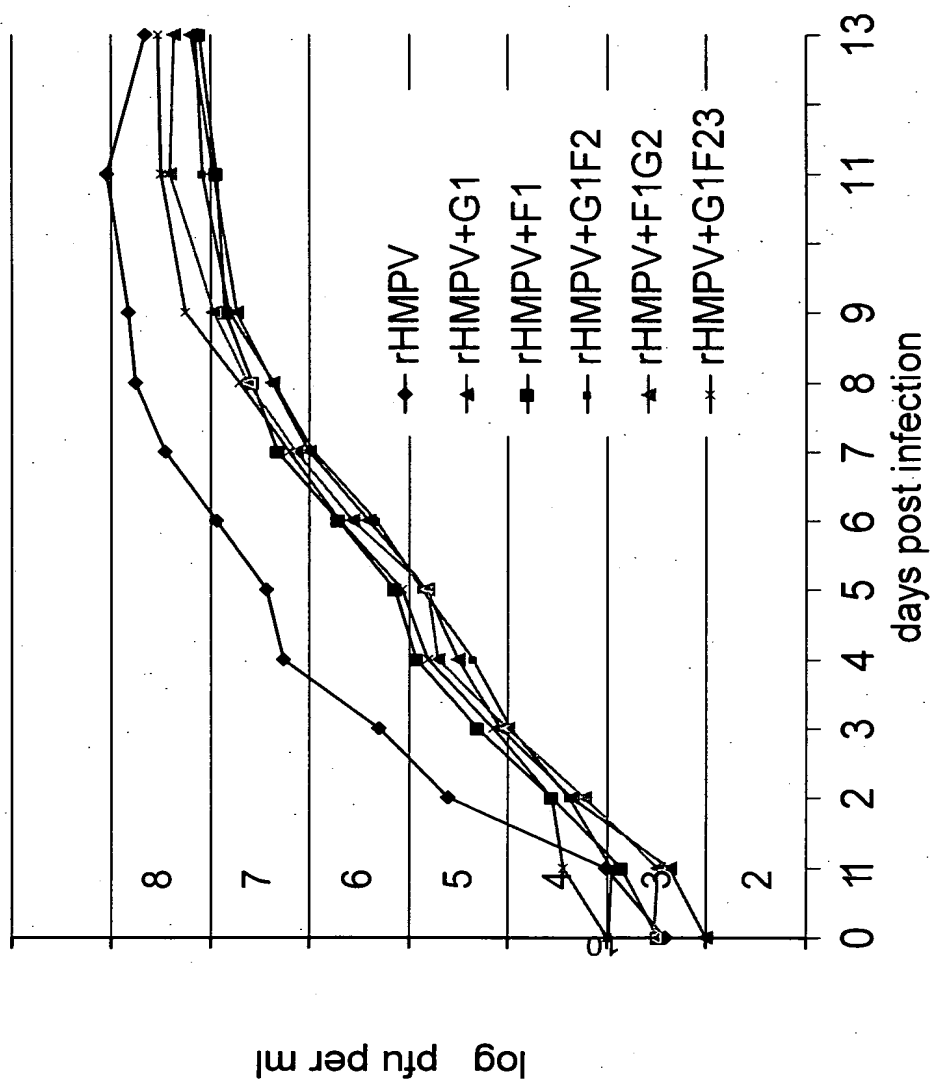


Fig. 25B

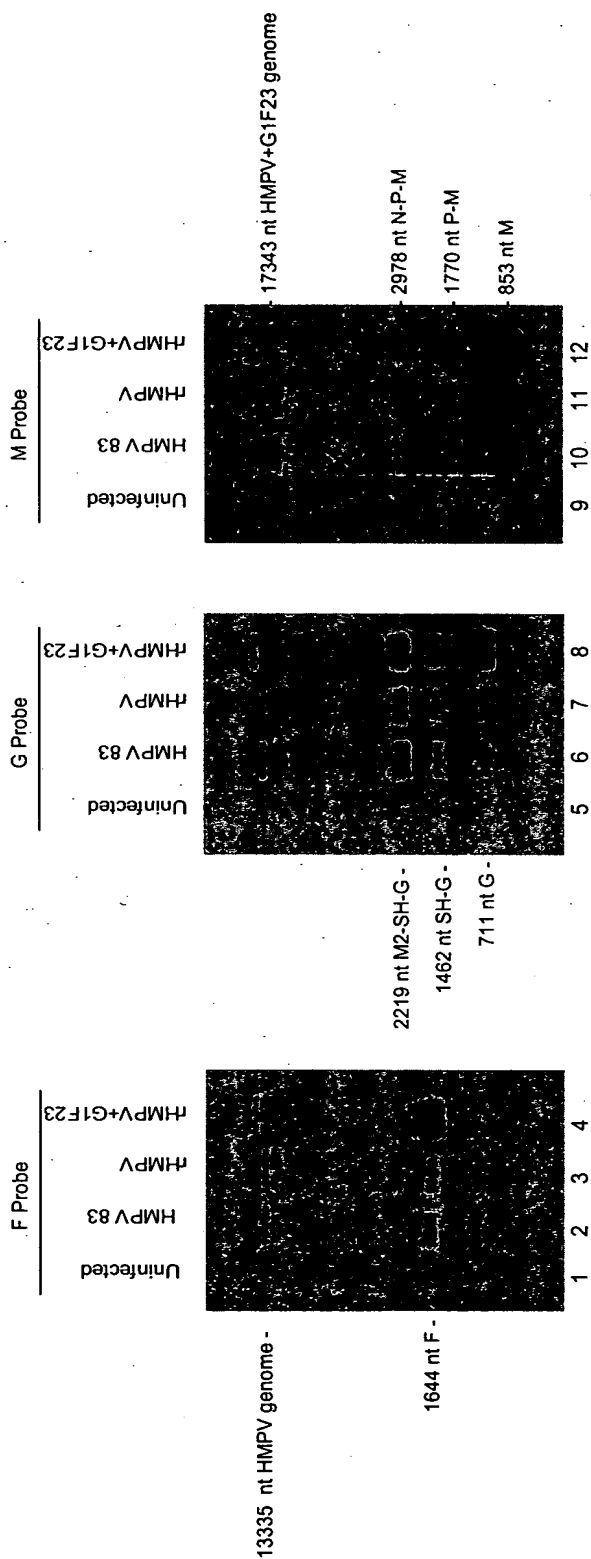


Fig. 25C

RSV A2 Mutations F521L and AA8

F521L (RSV)

hRSV A2	507	E	L	T	E	R	D	L	I	V	L	S	G	L	R	F	Y	R	E	F	R	L	P	K	V	D	L	E	M	I	I	N	D	K	A	I	S	P	P	K	N	L	I	W	T	-	S	F	P	R	
hPIV3	442	E	N	A	V	D	Y	Y	Q	S	F	I	G	I	K	F	N	K	F	I	E	P	Q	L	D	E	D	L	T	I	Y	M	K	D	K	A	L	S	P	P	K	-	S	N	W	D	T	V	Y	P	A
hPIV1	442	E	C	A	V	D	N	Y	S	S	F	I	G	F	K	F	L	K	F	I	E	P	Q	L	D	E	D	L	T	I	Y	M	K	D	K	A	L	S	P	P	K	-	A	A	W	D	S	V	Y	P	D
hMPV 83	442	E	L	S	E	Q	D	F	L	E	L	A	A	I	Q	F	E	Q	E	F	S	V	P	E	K	T	N	L	E	M	V	L	N	D	K	A	I	S	P	P	K	R	L	I	W	S	-	V	Y	P	K
hMPV 001	442	E	L	S	E	Q	D	F	L	E	L	A	A	I	Q	F	E	Q	E	F	S	V	P	E	K	T	N	L	E	M	V	L	N	D	K	A	I	S	P	P	K	R	L	I	W	S	-	V	Y	P	K

456

hRSV A2	593	N	Y	M	P	S	H	I	Q	N	Y	I	E	H	E	K	L	K	F	S	E	S	D	K	S	R	R	V	L	E	Y	Y	L	R	D	N	K	F	N	593
hPIV3	517	-	-	-	-	-	-	S	N	-	-	-	-	L	L	Y	R	T	N	A	S	N	E	S	R	R	L	V	E	V	F	I	A	D	S	K	F	D	517	
hPIV1	517	-	-	-	-	-	-	S	N	-	-	-	-	L	Y	Y	K	V	P	E	S	E	E	T	R	R	L	I	E	V	F	I	N	D	N	F	N	517		
hMPV 83	528	N	Y	L	P	E	T	I	K	N	R	Y	L	E	E	T	F	N	A	S	D	S	L	K	T	R	R	V	L	E	Y	Y	L	K	D	N	K	F	D	528
hMPV 001	528	N	Y	L	P	E	K	I	K	N	R	Y	L	E	E	T	F	N	A	S	D	S	L	K	T	R	R	V	L	E	Y	Y	L	K	D	N	K	F	D	528

456

hRSV A2	593	N	Y	M	P	S	H	I	Q	N	Y	I	E	H	E	K	L	K	F	S	E	S	D	K	S	R	R	R	V	L	E	V	Y	L	R	D	N	K	F	N	-	593
hPIV3	517	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	R	T	N	A	S	N	E	S	R	R	L	V	E	V	F	I	A	D	S	K	F	D	-	517
hPIV1	517	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	K	V	P	E	S	E	E	T	R	R	L	I	E	V	F	I	N	D	N	N	F	N	-	517
hMPV 83	528	N	Y	L	P	E	T	I	K	N	R	Y	L	E	E	T	F	N	A	S	D	S	L	K	T	R	R	R	V	L	E	V	Y	L	K	D	N	K	F	D	-	528
hMPV 001	528	N	Y	L	P	E	K	I	K	N	R	Y	L	E	E	T	F	N	A	S	D	S	L	K	T	R	R	R	V	L	E	V	Y	L	K	D	N	K	F	D	-	528

R588A
 D589A
 AA8 (double amino acid substitution)

Fig. 26A

HPIV3 Mutations Y942H and L992Y

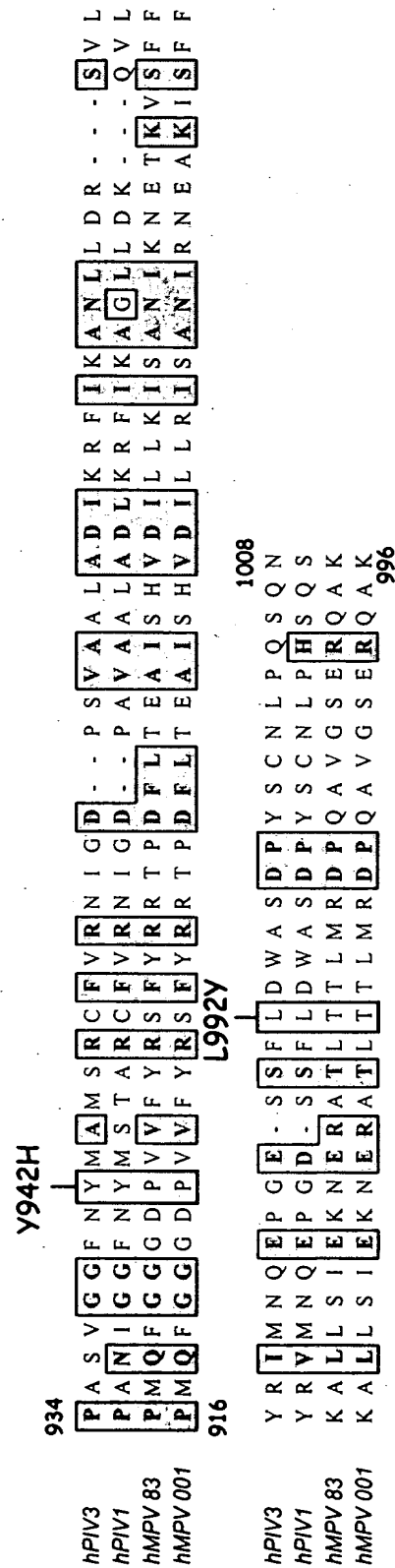


Fig. 26B

BPIV3 Mutation I1103V

I1103V

hPIV3	1087	R	V	G	I	S	R	R	G	-	G	L	T	Y	N	L	L	R	K	I	S	N	Y	D	L	V	Q	Y	E	T	L	S	1115
hPIV3	1087	R	V	G	I	N	R	R	G	-	G	L	T	Y	N	L	L	R	K	I	S	N	Y	D	L	V	Q	Y	E	T	L	S	1115
hPIV1	1087	R	A	S	V	R	R	G	-	G	L	T	Y	N	L	L	R	R	I	N	Y	D	L	V	Q	Y	E	T	L	S	1115		
hRSV A2	1153	K	T	S	A	I	D	L	T	D	I	D	R	A	T	E	M	M	R	K	N	I	T	L	L	I	R	I	L	P	L	1182	
hMPV 83	1078	R	T	S	A	I	N	G	E	D	I	D	R	A	V	S	M	M	L	E	N	L	G	L	L	S	R	I	L	S	V	1107	
hMPV 001	1078	R	T	S	A	I	N	G	E	D	I	D	R	A	V	S	M	M	L	E	N	L	G	L	L	S	R	I	L	S	V	1107	

HPIV3 Mutation T1558I

T1558I

hPIV3	1539	K	V	F	K	R	I	K	R	F	W	D	C	G	V	L	N	P	I	Y	G	P	N	T	A	S	Q	D	Q	I	K	L	A	L	S	I	C	E	1572		
hPIV1	1539	K	I	F	K	R	I	K	R	F	W	D	A	G	V	V	E	P	V	Y	G	P	N	L	S	N	Q	D	Q	I	L	L	A	L	S	I	C	E	1572		
hRSV A2	1586	K	V	I	K	Y	I	L	S	Q	D	A	G	V	V	L	V	S	L	H	S	F	K	N	H	S	F	K	N	W	F	I	L	K	R	L	S	V	A	E	1619
hMPV 83	1507	K	V	K	K	R	I	M	L	Y	D	V	K	F	L	S	L	F	L	S	L	V	G	Y	I	G	F	K	N	W	F	I	L	K	R	L	S	V	A	E	1540
hMPV 001	1507	K	V	K	K	R	I	M	L	Y	D	V	K	F	L	S	L	F	L	S	L	V	G	Y	I	G	F	K	N	W	F	I	L	K	R	L	S	V	A	E	1540

RSV A2 Mutation C319Y

C319Y

hPIV3	258	K	L	Q	S	M	Y	Q	K	G	N	N	L	W	E	V	I	D	K	L	F	P	I	M	G	E	K	T	F	D	V	I	288	
hPIV1	258	R	S	S	K	I	T	C	K	G	E	E	L	W	E	L	I	D	S	L	F	P	N	L	G	E	D	V	Y	N	I	I	288	
hRSV A2	302	R	C	G	F	N	N	V	I	L	T	Q	K	L	F	L	Y	G	D	C	I	L	K	L	F	H	N	E	G	F	Y	I	I	332
hMPV 83	239	R	S	N	L	Q	G	M	L	T	N	K	L	L	Y	E	T	V	D	Y	M	L	S	L	C	C	N	E	G	F	S	L	V	269
hMPV 001	239	R	S	N	L	Q	G	I	L	T	N	K	L	L	Y	E	T	V	D	Y	M	L	S	L	C	C	N	E	G	F	S	L	V	269

Fig. 26C

RSV A2 Mutation Q831L

hPIV3	772	G D N Q A I A V T T R V P N N Y D Y R I K K E I V Y K D D V V R F F D S L R E V M D D L G H	816
hPIV1	772	G D N Q A I A V T T S R V P V T Q T Y K Q K K T H V Y E E I T R Y F G A L R E V M F D I G H	816
hRSV A2	810	G D N Q S I D I S K P I R L M E G Q T - H A Q A D Y L L L A L N S L K L L Y K E Y A G I G H	853
hMPV 83	744	G D N Q S I D V S K P V K L S E G L D - E V K A D Y R L A V K M L K K E T R D A Y R N I G H	787
hMPV 001	744	G D N Q S I D V S K P V K L S E G L D - E V K A D Y S L A V K M L K K E T R D A Y R N I G H	787

RSV A2 Mutations M1169V, D1183E and C9

hPIV3	1087	R V G I N R R G - G L T Y S L L R R K I S N Y D D L V Q Y E T L S R T L R	D1183E
hPIV1	1087	R A S V R R G - G L S Y S I L L R R L I N Y D D L L L Q Y E T L T R T L R	
hRSV A2	1153	K T S A I D L T I D R A T E M M R K E N L G G L L L R I L P L D C N R	
hMPV 83	1078	R T S A I N G E D I D R A V S M M L E N L G G L L L R I L S V V V D S	
hMPV 001	1078	R T S A I N G E D I D R A V S M M L E N L G G L L L R I L S V V V D S	

hPIV3	1160	L I V S D K I R Y E D M C S V D L A I A L R Q K M W I H L S G G R M I S G L E T P	1160
hPIV1	1160	K P V K D N I E Y E M C S V E L A I G L R Q K M W F H L T Y G R P I H G L E T P	1160
hRSV A2	1222	D K R E I L S M E N L S I - T E L S K Y V R E R S W S L S N - - - I V G V T S P	1222
hMPV 83	1147	I E I P I K S N G R L I C - C Q I S R T L R E T S W N N M E - - - I V G V T S P	1147
hMPV 001	1147	I E I P I K S N G R L I C - C Q I S R T L R E T S W N N M E - - - I V G V T S P	1147

D1187A* R1189A*
 K1188A* E1190A*
 E1208A* R1209A*

* Six point mutations collectively designated C9

hPIV3	1249	W A F G	E I	S W M E	A S	Q	I A Q T R	A N F T L	S L K I	P V A T S	N L S	H R L	1292
hPIV1	1249	W A Y G	E I	S W M E	A A	L	I A Q T R	A N F T L	S L K I	P V S T S	N L S	H R L	1292
HRSV A2	1297	W V Y A	S I	D N K D	E F M	E E	I G T L	G L T Y E	K A K K	Y L S V N	Y L S	H R L	1340
hMPV 83	1222	W V Y K	G T P	G L R R	L L	N K	I C L G S	L G I S Y K	C V K P	F M S V N	F L S	H R L	1265
hMPV 001	1222	W V Y K	G T P	G L R R	L L	N K	I C L G S	L G I S Y K	C V K P	F M S V N	F L S	H R L	1265

RSV A2 Mutation H1690Y

hPIV3	1626	P	N	L	N	L	T	Y	L	E	R	D	L	S	K	Q	Y	L	E	N	I	K	E	D	P	-	-	-	-	-	-	T	L	K	Y	V	Q	I	S	G	L	I	K	S	F	P	S						
hPIV1	1626	P	K	L	E	S	M	T	S	L	E	R	L	E	S	L	K	E	Y	L	E	L	T	F	L	D	D	D	P	-	-	-	-	-	-	I	L	R	Y	S	Q	I	L	T	G	L	V	I	K	I	F	P	S
hRSV A2	1673	L	F	Y	I	N	Y	N	F	S	D	N	T	H	L	T	K	H	I	R	I	A	N	S	E	L	E	B	N	N	Y	N	K	L	Y	H	P	T	P	E	T	L	E	N	I	L	A	N	P	I	K	S	
hMPV 83	1573	L	R	I	T	V	L	N	Y	T	D	M	A	H	A	L	T	R	L	I	R	K	K	-	-	-	-	-	-	-	-	-	-	-	-	L	M	C	D	N	A	L	L	T	P	I	S	S					
hMPV 001	1573	L	R	I	T	V	L	N	Y	T	D	M	A	H	A	L	T	R	L	I	R	K	K	-	-	-	-	-	-	-	-	-	-	-	L	M	C	D	N	A	L	L	T	P	I	P	S						

RSV A2 Mutation N43I

hPTV3	24	I	V	K	G	K	I	A	Q	L	H	T	I	M	S	L	P	Q	P	Y	D	M	D	D	S	I	L	V	I	52	
hPTV1	24	I	V	K	S	K	I	A	Q	L	H	V	L	L	D	I	N	Q	P	Y	D	L	K	D	N	S	I	I	N	I	52
hRSV A2	23	I	S	F	S	E	C	N	A	L	G	S	Y	I	-	F	N	G	P	Y	L	K	N	D	Y	T	N	L	I	S	50
hMPV 83	22	I	S	F	S	E	T	N	A	I	G	S	C	L	-	L	K	R	P	Y	L	K	N	D	N	T	A	K	V	A	49
hMPV 001	22	I	S	F	S	E	T	N	A	I	G	S	C	L	-	L	K	R	P	Y	L	K	N	D	N	T	A	K	V	A	49

N43I

BPIV3 Mutation T1711I

bPIV3	1690	P	E	T	I	E	D	W	D	P	I	E	D	E	N	I	L	D	D	N	I	V	K	T	V	N	D	N	C	S	D	N	Q	K	R	N	K	S	S	Y	F	W	1729	
hPIV3	1690	P	E	V	I	D	D	W	D	P	I	E	D	E	N	M	L	D	D	N	I	V	K	T	I	N	D	N	C	C	N	K	D	N	K	G	N	K	I	N	N	F	W	1729
hPIV1	1690	P	E	V	L	E	D	W	D	P	I	D	A	S	M	L	L	D	D	N	I	T	A	E	V	Q	H	N	I	P	-	-	L	K	N	E	R	T	P	F	W	1727		
hRSV A2	1744	P	L	L	S	N	K	K	L	I	K	S	S	A	M	I	R	T	Q	V	N	Y	S	K	Q	L	N	N	L	-	-	-	-	-	-	-	-	-	-	-	F	P	1772	
hMPV 83	1608	P	M	V	N	-	-	-	-	-	-	-	-	-	-	L	T	Q	V	I	D	P	P	T	Q	L	D	Y	-	-	-	-	-	-	-	-	-	-	-	-	F	P	1626	
hMPV 001	1608	P	M	V	N	-	-	-	-	-	-	-	-	-	-	L	T	Q	V	I	D	P	P	T	Q	L	A	Y	-	-	-	-	-	-	-	-	-	-	-	-	F	P	1626	

T1711I

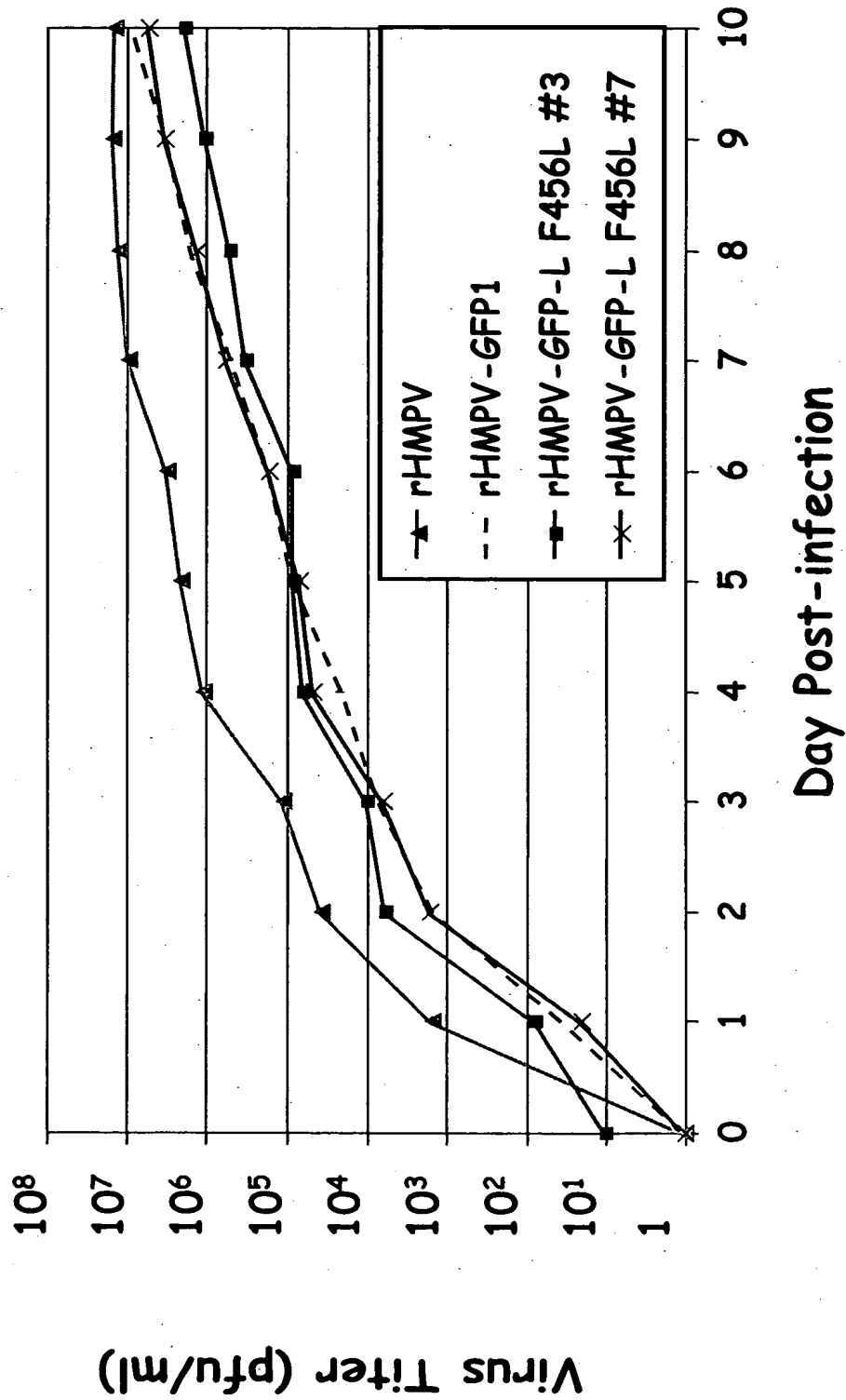


Fig. 27

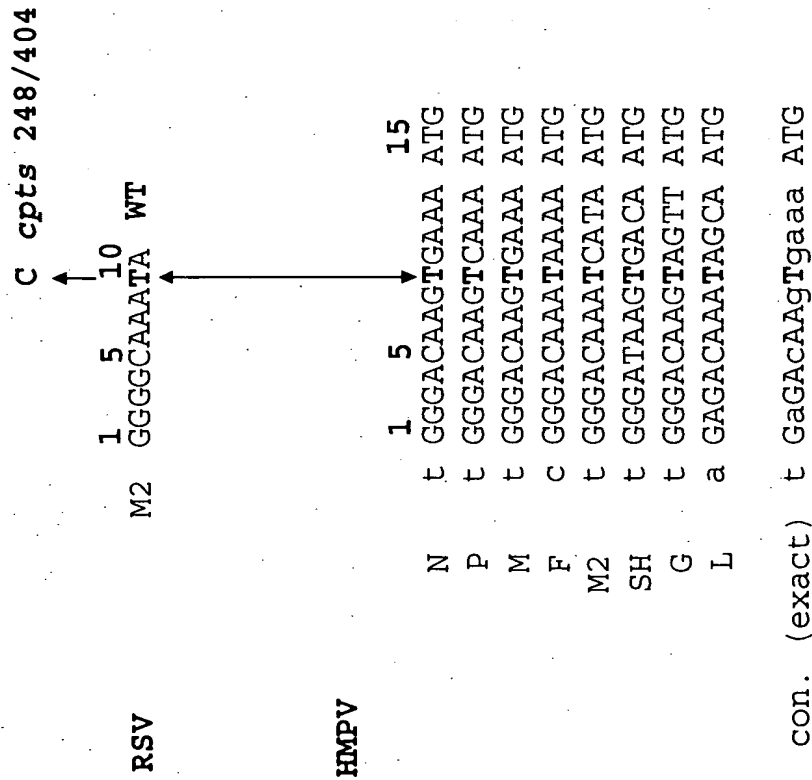
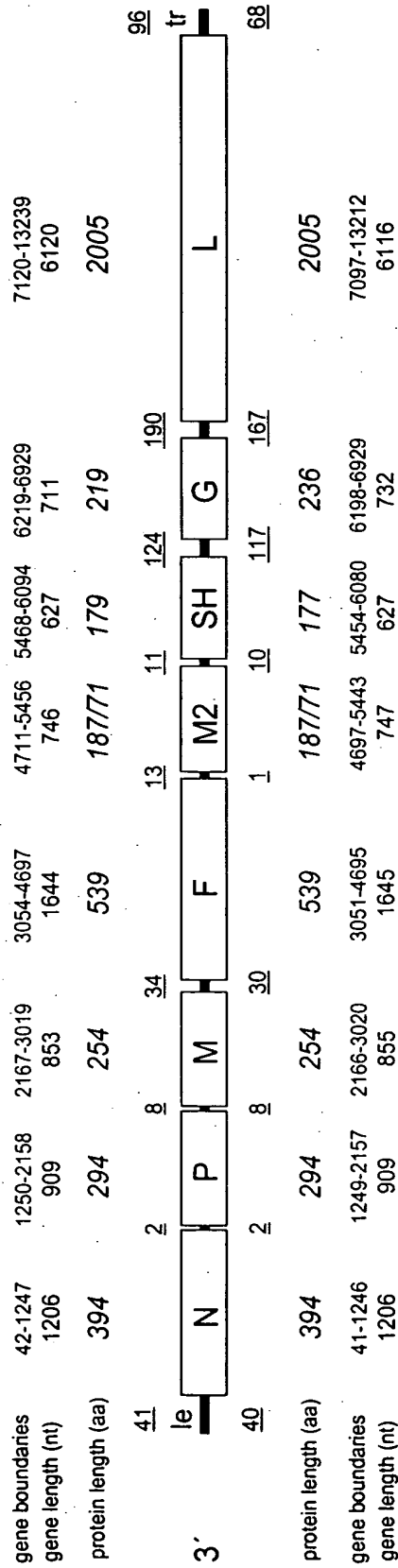


Fig. 28

CAN97-83, 13,335 nucleotides



CAN98-75, 13,280 nucleotides

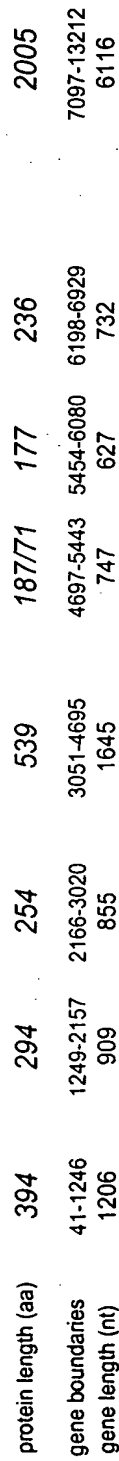


Fig. 29

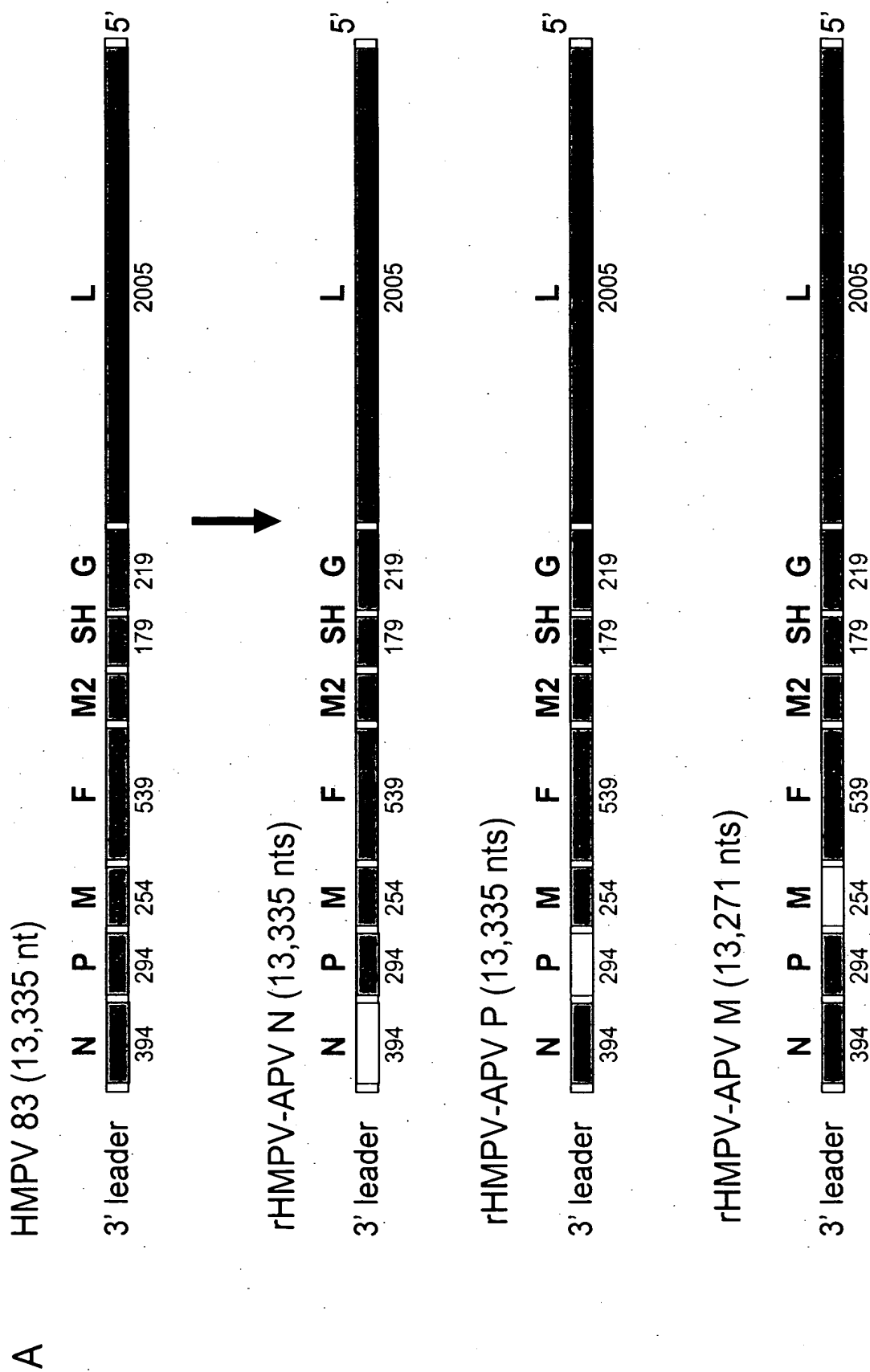


Fig. 30A

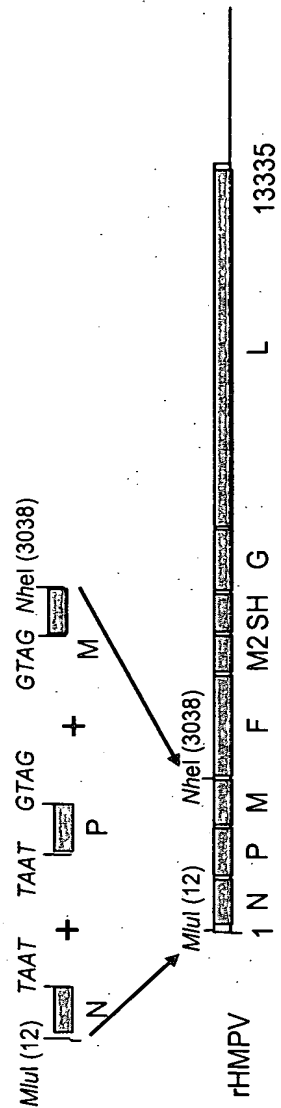
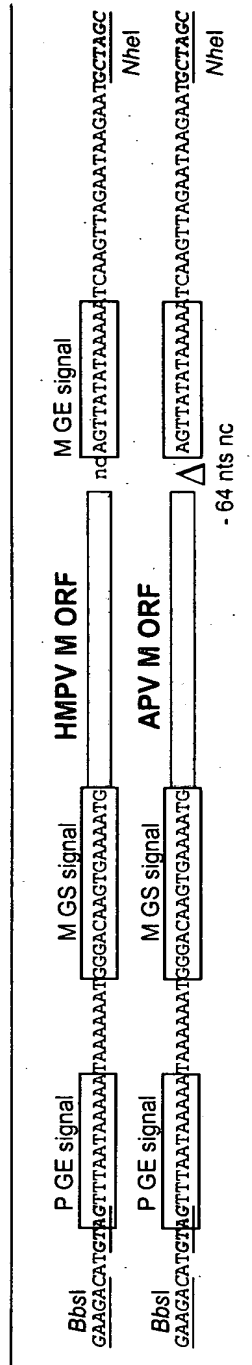
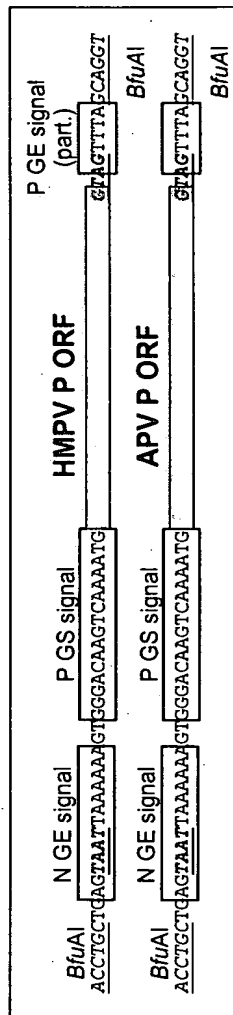
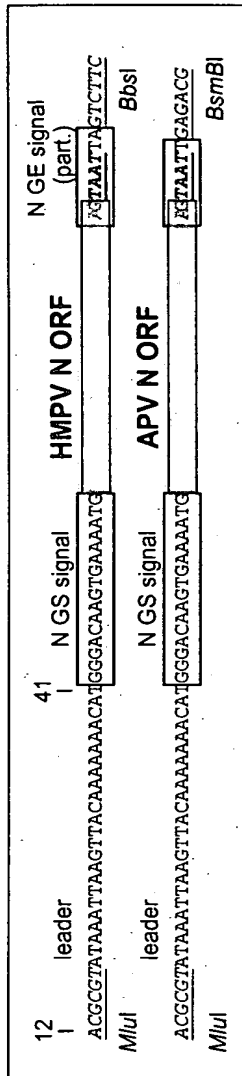


Fig. 30B-E

	gene-end	intergenic	gene-start
	1 13		1 16
le (83)	aattaAGTTAcaaaaaacat		GGGACAAgTgAAaATGtctct N (83)
(75)	aattaAaTTccaaACAAAAC-		GGGACAAaTaAAaATGtctct (75)
N (83)	ttatgAGTAAttaAAAA--	gt	GGGACAAgTcAAaATGtctct P (83)
(75)	ttatgAGTAAttaAAAA--	ct	GGGACAAgTcAAaATGtctct (75)
P (83)	tatgtAGTTtaataAAAA--	taaaaaat	GGGACAAgTgAAaATGgagtc M (83)
(75)	catgtAGTTtaataAAAA--	taacaat	GGGACAAgTcAagATGgagtc (75)
M (83)	atattAGTTAtatAAAA--	tcaag- 24 nt-agaac	GGGACAAaTaAAaATGtcttg F (83)
(75)	attatAGTTAtatAAAAAA	tttag- 20 nt-aaagc	GGGACAAgTaAAaATGtcttg (75)
F (83)	cagttAGTTAattAAAA--	taaaataaaaattt	GGGACAAaTcATaATGtctcg M2 (83)
(75)	tagttAGTTAattAAAAAA-	t	GGGACAAaTcATcATGtctcg (75)
M2 (83)	acttaAGTTAgtaAAAA--	cacatcagagt	GGGATAAGTgACaATGataac SH (83)
(75)	acttaAGTTAgtaAAAA--	taaatagaat	GGGATAAAaTgACaATGaaaaac (75)
SH (83)	agtttAGTTAttttAAAA--	tattt-114 nt-aatat	GGGACAAgTagttATGgaggt G (83)
(75)	agtctAGTTAttttAAAA--	ctcta-107 nt-aaaat	GGGACAAgTggccATGgaagc (75)
G (83)	aaattAGTTAacaAAAA--	tacga-180 nt-tccaa	GaGACAAaTagcAAATGgatcc L (83)
(75)	caagtAGTTAacaAAAAAA-	ctata-157 nt-ttcaa	GGGACAAaTaacaATGgatcc (75)
L (83)	atgatAGTTAattAAAA--	ttaaa-91 nt	tr (83)
(75)	ccattAGTTAattAAAA--	ttata-63 nt	(75)
consensus	AGTTAnnnAAAAA		GGGACAAAnTnnnAAATG

Fig. 31

Percent amino acid or nucleotide sequence identity between the indicated strains of HMPV or RSV for the indicated proteins and ORFs

Viruses compared	percent amino acid sequence identity for indicated protein (percent nucleotide sequence identity for indicated ORF)								
	N	P	M	F	M2-1	M2-2	SH	G	L
CAN97-83 vs CAN98-75	96 (84)	85 (81)	97 (85)	95 (84)	96 (85)	89 (87)	59 (69)	37 (59)	94 (84)
CAN97-83 vs 00-1	99 (94)	95 (92)	99 (94)	98 (94)	98 (94)	96 (95)	85 (88)	70 (77)	99 (95)
RSV A2 vs RSV B1	95 (85)	90 (85)	91 (85)	89 (81)	91 (84)	61 (69)	72 (77)	55 (67)	92 (85)

A. SH protein

CAN98-75	1	K		E	NQ	K	L	S	PT	S	V	V	T	54		
CAN97-83	1	MITLDVIKSDGSSKTCTHLKLIKDHSGKVLIALKLILALLTFFTTITINYIK												54		
00-1	1	V L V ***** *.****.* *												54		
* ***** **...***** ***** *																
CAN98-75	55	A	L	N		K	TKL		T	IRPI	LNAV	L	KH	N	TKD	108
CAN97-83	55	VENNLQICQSKTESDKEDSPSNTTSVTKTLDHDITQYFKRLIQRYTDSVIN-														107
00-1	55	K SS N SL TN A -														107
***** ** *.***** *. **** * . ** * ****. * *																
CAN98-75	109	R	R	HT		KI	GSMN	TND	E	E	P	V	DK	TMT	KHRKA	162
CAN97-83	108	KDTCKISRNOCTNITTYKFLCFKPEDSKINSCDRLTDLCRNKSAAEAYHTV														161
00-1	108	S	N				S	T	N	K		P	P	VG	I	161
*****. * ***** ***** . . * . * * * *																
CAN98-75	163	RPH T W HYL----- 177														
CAN97-83	162	ECHCIYTIEWKCYHHSID---- 179														
00-1	162	VK YPT ETQS 183														
*** * * * *																

Fig. 33A

B. G protein

CAN98-75	1	AR	F	KM	IRS	HR	T	S	AP	M	TL	DHA	54
CAN97-83	1	MEVKVENIR	RAIDML	KARVKNR	VARSKCFK	NASL	ILIGIT	TL	SL	AL	NI	YLI	54
00-1	1	T				V						K	54
		**	*****	***	****	***	***	***	*	***	***	***	
CAN98-75	55	TS	NMTKV	CVNM	V	PS	KTPMT	AAD	NTK	P	QA	LT	DS
CAN97-83	55	IQKTSS	SESEHHT	SSPPTES	KNKEAST	ISTD	NPDP	INPNS	QHP	TQQ	STEN	PTLN	PAA
00-1	55	M	NT	S	M	SR	TP	VP	S	T	SSP	GS	YF
		**	**	*	*	*	*	*	*	*	*	*	*
CAN98-75	109	LEDHLH	GTTP	A	VSQQT	EH	TLLRSTNRQ	TQ	TAEKKP	TRAT	TKKET	162	
CAN97-83	109	SVPSE	TEPAST	PD	TNRLSS	VDR	STAQP	SESR	TKTKPT	VHTR	NNP	STAS	TQS
00-1	109	A	SP	T	PPF	TH	TP	A	S	A	K	R	S
		*	***	*	*	*	*	*	*	*	*	*	*
CAN98-75	163	TT	T	ST	ATQTLN	TNTNQ	TSNG	EA	AR	RNNA	SSDQ	TQ	ADPS
CAN97-83	163	PPRAT	TKAIR	RAT	TFRMS	STGKR	-PTT	SVQSD	SS	TTTQ	NHEET	GSAN	POASVS
00-1	163	RTA	T	L	T	R	-S	A	P	I	A	HKN	ASP
		*	*	*	*	*	*	*	*	*	*	*	*
CAN98-75	217	QHTQK	STTT	THNTD	TSSP	SS	-	236					
CAN97-83	216	TMQN	-----	219									
00-1	216	TRIQR	KSVEAN	TSTTYN	QTS	236							

Fig. 33B

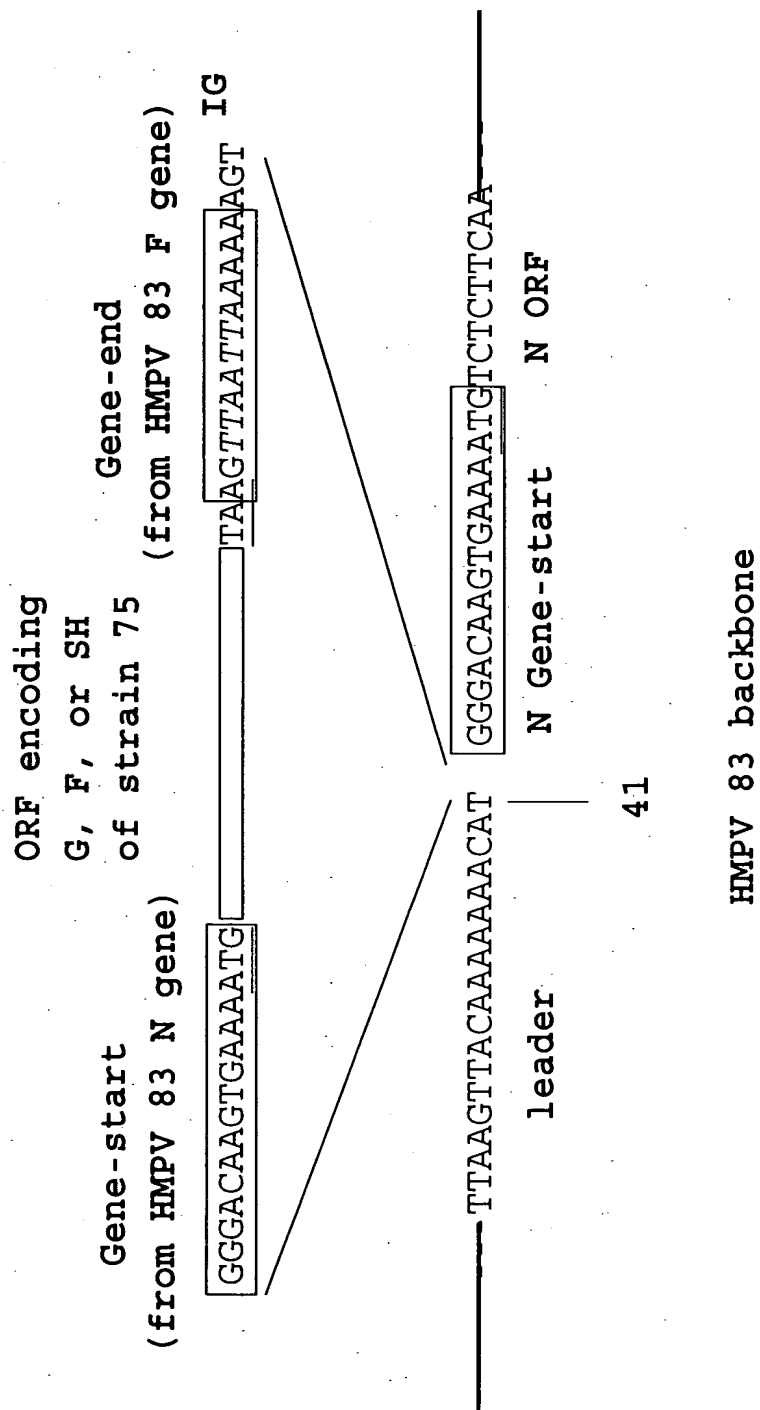


Fig. 34

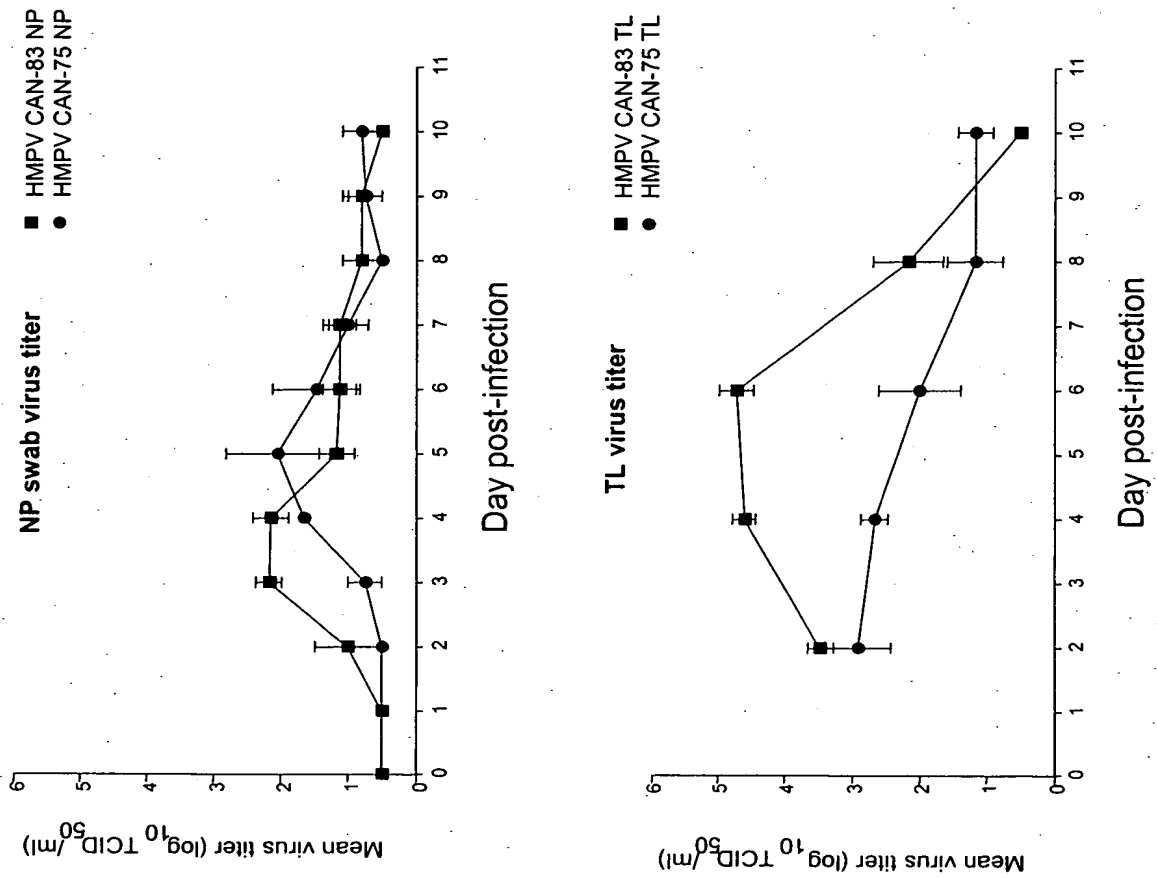


Fig. 35

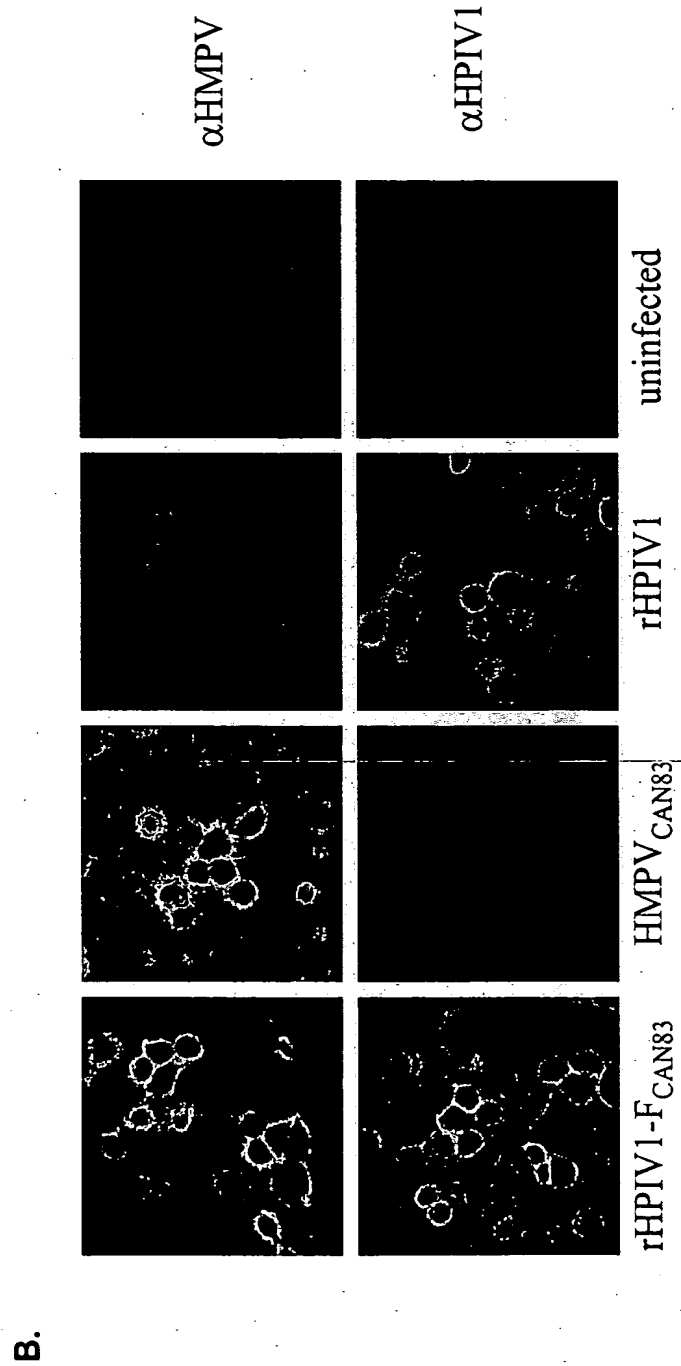
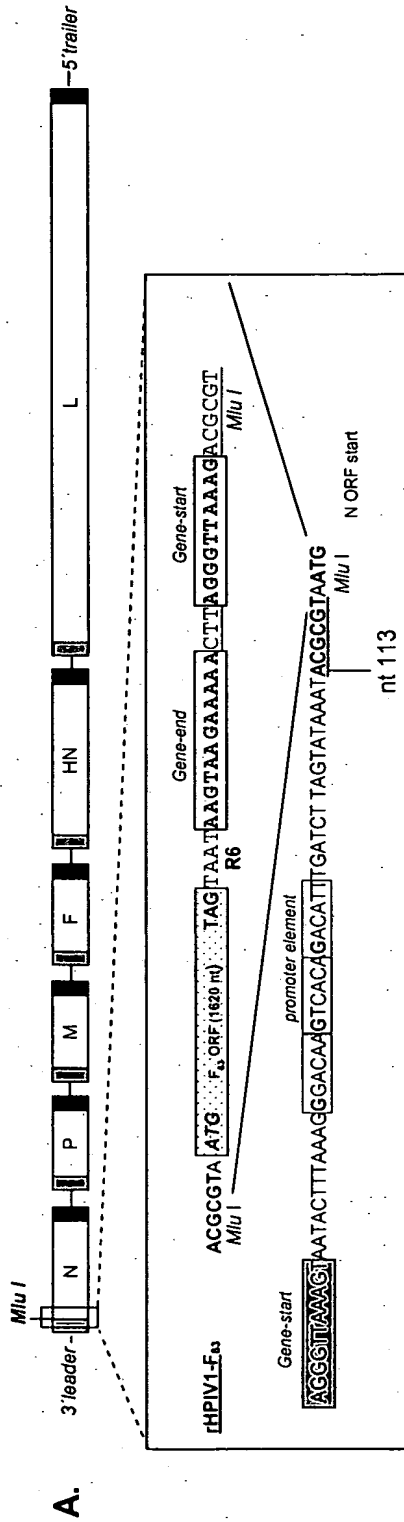


Fig. 36A & B

HMPV strain 83

1	ACGCGAAAA	AACGGGTATA	AATTAAGTTA	CAAAAAAACA	TGGGACAAGT	50	GAATAATGCT	CTTCAAGGGA	TTCACTGAG	TGATCTATCA	TACAAGCATG	100
101	CTATATATA	AGAGTCTCAG	TATACAATA	AGAGATATGT	AGGCAACAAC	60	ACAGCATGA	CACCTCATC	ATTCAACAA	GAATACAC	TATTGTGTG	200
201	AGAAATCTA	TATGCTAAG	ATGCTGATTA	CAATATATGT	GCAGAAATAG	70	GAATACATA	TATTAGCACA	CTCTAGGAT	CAGAGAGAT	ACAGCAGAT	300
301	CTAAGAACT	CAGGCAGTGA	AGTCCAAGTG	GTTTAAACCA	GAACGFACTC	80	CTTGGGAAA	GTTAAAAACA	ACAAAGGAGA	AGATTTACAG	ATGTTAGACA	400
401	TACACGGAGT	AGAGAAAGC	TGGGTGGAAG	AGATAGACAA	AGAAGCAAGA	90	AAAAACATGG	CAACTTTGCT	TAAAGAATCA	TCAGGCAATA	TTCCACAAAA	500
501	TCAGAGGCTT	TCAGACCCAG	ACACACCTAT	AATCTTATTA	TGTGTAGGTG	100	CCTTAATATT	TACCAAACTA	GCATCAACTA	TAGAAGTGGG	ATTAGAGACC	600
601	ACAGTCAGAA	GAGCTAACCG	TGTACTAAGT	GATGCACTCA	AAAGATACCC	110	TAGGATGGAC	ATACCAAAAA	TCGCTAGATC	TTTTCTATGAT	TTATTTGAAC	700
701	AAAAAGTGTA	TTACAGAAAT	TTGTTTCAATG	AGTATGGCAA	AGCATTAGGC	120	TCATCTCTTA	CAGGCAGCAA	AGCAGAAAGT	TTATTCCTTA	ATATATTCAAT	800
801	GCAAGTTTAC	GGTGTGGTC	AAACAATGCT	GAGTGGGGA	GTCAATTGCCA	130	GGTCATCTAA	CAATATAATG	TTAGGACATG	TATCTGTCCA	AGCTGAGTTA	900
901	CAACAGTTCA	CAGAAGTCTA	TGACCTGGTG	CGAGAAATGG	GCCCTGAATC	140	TGGCTCCTTA	CAATTAAGGC	AAAGCCCAA	AGCTGGACTG	TTATCACTAG	1000
1001	CAACTTTGCC	CAACTTTGCC	AGTGTGTTTC	TCGGCAATGC	CTCAGGCTTA	150	GGCATATAG	GTATGTATCG	CGGAGAGATG	CCAAACACAG	AACTATTTTC	1100
1101	AGCAGCAGAA	AGCTATGCCA	AGAGTTTGAA	AGAAAGCAAT	AAAAATTAAT	160	TTTCTTCATT	AGGACTCACA	GATGAAGAAA	AAAGGCTGC	AGAACACTTT	1200
1201	CTAATGTGA	GTGACGACAG	TCAAAATGAT	TATGAGTAAT	TAAAAAAGTG	170	GGACAAGTCA	AAATGTCTAT	CCCTGAAGGA	AAAGATATTC	TTTTCATGG	1300
1301	TAATGAAGCG	GCAAAATGG	CAGAAGCTTT	CCAAAAATCA	TTAAGAAAAC	180	CTAGTCATAA	AAATCTCAA	TCTATTATAG	GAGAAAAGT	GAACACTGTA	1400
1401	TCTGAACAT	TGGAATTACC	TACTATCAGT	AGACCTACCA	AACCGACCAT	190	ATTGTACAG	CCGAAGTTAG	CATGGACAGA	CAAAGTGGG	GCAATCAAAA	1500
1501	CTGAAGCAAA	GCAACCAATC	AAAGTTATGG	ATCCTATTGA	AGAAGAAGAG	200	TTTACTGAGA	AAAGGTTGCT	GCCCTCCAGT	GATGGGAAA	CTCCTGCAGA	1600
1601	AAAGAGTTTG	AAACCACTCA	CCAATACTAA	AAAGAAGGTC	TCAATTTACAC	210	CAAAATGAAC	AGGAAAATAC	ACAAAGTTGG	AGAAAGATGC	TCTAGACTTG	1700
1701	CTTTACAGTA	ATGAAGAGA	AGATGCAGAA	TCCTCAATCT	TAACCTTCTGA	220	AGAAAGAGAT	ACTTCATCAT	TAAGCATTTG	AGCCAGACTA	GAATCGATTG	1800
1801	AGGAGAAAT	AAGCATGATA	TTAGGGCTAT	TAAAGAACT	CAACCTTGCT	230	ACAGAGACAT	CCACATGAGT	AGAGATGGG	ATCCAGAGATG	CAATGATTGG	1900
1901	CATAGGGGAG	GAACTAATAG	CAGACATAT	AAAGAAGCC	AAGGGAAGAG	240	CAGCAGAAAT	GATGGAAGAA	GAATGAACC	AGCGGACAAA	AATAGGAAC	2000
2001	GGTAGTGTA	AATTAAGTGA	AAAGGCAAG	GAGCTCAACA	AAATTTCTGA	250	AGACGAGAGC	ACAAGTGTG	AATCGGAAGA	AGAAGAAGAA	CTAAAAGACA	2100
2101	CACAGGAAA	TAATCAAGAA	GATGACATTT	ACCAGTTAAT	TATGTAGTTT	260	AATAAATA	AAAAATGGGA	CAAGTGAATA	TGGAGTCTTA	TCTGGTAGAC	2200
2201	ACCTATCAAG	GCATCCCTTA	CACAGCAGT	GTTCAAGTTG	ATCTAGTAGA	270	AAAGGACCTG	TTACCTGCNA	GCCTAACAAT	ATGGTTCCCC	CTGTTTCAGG	2300
2301	CCAATACACC	ACCAGCAGTT	CTGCTTGATC	AGCTAAAGAC	TCTGACTATA	280	ACTACTCTGT	ATGCTGCATC	ACAAAGTGGT	CCAATACTAA	AGTGAATGC	2400
2401	ATCGGCCAG	GGTGCAGCAA	TGCTGTACT	TCCCAAAAAA	TTTGAAGTCA	290	ATGCGACTGT	AGCAGTTGAC	GAATATAGCA	AATTAGAATT	TGACAAACTT	2500
2501	ACAGTCTGTG	AGTAAAAAC	AGTTTACTTA	ACACCATGA	AACCATATGG	300	GATGGTATCA	AGTTTGTGA	GCTCGGCCAA	ACCAGTTGGC	AAAAAACAC	2600
2601	ATGATCTAAT	CGCATTTATG	GATTTTATGC	TAAGTATGG	ATCTAGAAA	310	GTTACATAC	CAGCATTTAT	CAATCAGTT	TCTATCAAG	AGAGTGAATC	2700
2701	AGCCACTGTT	GAAGCTGCAA	TAAGCAGTGA	AGCAGACCAA	GCTCTAACAC	320	AAGCCAAAAT	TGCACCTTAT	GCGGACTGA	TCATGATTAT	GACCATGAAC	2800
2801	AATCCCAAAG	GCATATTCAA	GAAGCTTGA	GCTGGGACCC	AAGTTATAGT	330	AGAACTAGGA	GCATATGTCC	AGGCTGAAAG	CATAAGTAAA	ATATGCAACA	2900
2901	CTTGGAGCCA	TCAAGGAACA	AGATATGTG	TGAAGTCCAG	ATAACAGCCA	340	AGCAACTGA	CCAAAGAACTA	CCAACTCTAT	TCTATAGACT	AAAAAGTCGC	3000
3001	CATTTTAGTT	ATATAAAAT	CAAGTTAGAA	TAAGAAATTA	ATCAATCAAG	350	AACGGGACAA	ATAAAAATGT	CTTGGAAAAGT	GGTGAATCAT	TTTTTCATGC	3100
3101	TAATAAACACC	TCAACACGGT	CTTAAAGAGA	GCTACCTAGA	AGAATCATGT	360	AGCACTATAA	CTGAGGGATA	TCTTAGTGT	CTGAGGACAG	GTTGGTATAC	3200
3201	CAACGTTTTT	ACATTAGAGG	TGGGTGATGT	AGAAAACCTT	ACATGTTCTG	370	ATGGAACCTAG	CCTAATAAAA	ACAGAATTAG	ATCTGACCAA	AAGTGCACTA	3300
3301	ATGAGACCTCA	AAACAGTCTC	TGCTGACCAA	TTGGCAAGAG	AGGAACAAAT	380	TGAGAACTCC	CGAAATCTA	GGTTGTTCT	AGGAGCAATA	GCATCGGTG	3400
3401	TTGCAACAGC	AGCTGCAGTC	ACAGCAGGTG	TTGCAATTGC	CAAAACCATC	390	CGGCTTGAGA	GTGAACATCA	AGCAATTAAG	AATGCCCTCA	AGACGCCAA	3500
3501	TGAAGCAGTA	TCTACATTTG	GGAATGGAGT	TCGAGTGTG	GCAACTGCAC	400	TGAGAGAGAT	GAAAGACTTT	GTGAGCAAG	ATTTAACTGC	TTGCAATCAAC	3600
3601	AAAAACAAGT	GCGACATTTA	TGACCTAATA	ATGGCCGTTA	GCTTCAGTCA	410	ATTCACAGTA	AGGTTCTTAA	ATGTTGTGCG	GCAATTTTCA	GACAATGCTG	3700
3701	GAATAACACC	AGCAATATCT	TTGGACTTAA	TGACAGATGC	TGAACCTAGCC	420	AGGCCCGTTT	CTAACATGCC	GACATCTGCA	GGACAAATAA	AATTGATGTT	3800

Fig. 37A

HMPV strain 83 (continued)

3801	GGAGAACCGT	GGCATGGTGC	GAAGAAAGGG	GTTCCGAATC	CTGATAGGGG	TCTACGGGAG	CTCCGTAATT	TACATGGTGC	AGCTGCCAAT	CTTTGGCGTT	3900
3901	ATAGACACGC	CTTGCTGGAT	AGTAAAGCA	GCCCTTCTT	GTTCCGAAAA	AAAGGGAAC	TATGCTTGCC	TCCTTAAGAG	AGACCAAGGG	TGGTATTGTC	4000
4001	AGAATGCAGG	GTCAACTGTT	TACTACCCAA	ATGAGAAAG	CTGTGAAGAA	AGAGGAGACC	ATGCTTTTGG	CGACACAGCA	CGGGAATTA	ATGTTGCTGC	4100
4101	GCAATCAAA	GAGTGCACAA	TCAACATATC	CACATCAAT	TACCCATGCA	AAGTCAGCAC	ATGGAAGACAT	CCTATCAGTA	TGGTTGCACT	GTCTCCTCTT	4200
4201	GGGGCTCTGG	TTGCTTGCTA	CRAAGGAGTA	AGCTGTTCCA	TTGGCAGCAA	CAGAGTAGGG	ATCATCAAGC	AGCTGAACAA	GGTTGTCTCC	TATATAACCA	4300
4301	ACCAAGATGC	AGACACAGTG	ACATAGACA	ACACTGTATA	TCAGCTAAGC	AAAGTTGAGG	GTGAACAGCA	TGTTATAAAA	GGCAGACCAG	TGTCAAGCAG	4400
4401	CTTTGATCCA	ATCAAGTTTC	CTGAAGATCA	ATTCATGTT	GCACTTGACC	AAAGTTTGA	GAACATTGAA	AACAGCCAGG	CCTTGGTAGA	TCAATCAAA	4500
4501	AGAATCCCTAA	GCAGTGCAGA	GAAGGGAAT	ACTGGCTTCA	TCATTGTAAT	AATTCTAATT	GCTGTCTTGG	GCTCTAGCAT	GATCCTAGTG	AGCATCTTCA	4600
4601	TTATTAATCAA	GAACCAAAAG	AAACCAACGG	GAGCACTCC	AGAGCTGAGT	GGGTGCACAA	ACAATGGCTT	CATACACAC	AGTTAGTTAA	TTAAAAATAA	4700
4701	AATAAAATTT	GGGACAAATC	ATAATGTCTC	GCAAGGCTCC	ATGCAATAT	GAAGTCGGG	GCAATGGCAA	CAGAGGAAGT	GAGTGTAAAT	TTAACCAACA	4800
4801	TTACTGGAGT	TGGCCAGATA	GATACTTATT	AATAAGATCA	AACTATCTAT	TAAATCAGCT	TTTAAAGGAA	ACTGATAGAG	CTGATGSCCT	ATCAATAATA	4900
4901	TCAGGCGCAG	GCAGAGAGAA	CAGAACGCAA	GAATTTGTTT	TAGGTTCCAC	CAATGTGGTT	CAAGGTTATA	TTGATGATAA	CCAAAGCAT	ACAAAAGCTG	5000
5001	CAGCTGTGTA	CAGCTACAC	AACATAATCA	AGCAACTACA	AGAAGTTGAA	GTTAGGCAGG	CTAGAGATAG	CAAACTATCT	GACAGCAAGC	ATGTGGCACT	5100
5101	CCATAACTTA	ATCTTATCTT	ACATGGAGAT	GAGCAAACT	CCCGATCTT	TAATCAACAA	TCTCAAAAGA	CTGCCAGAG	AAAACTGAA	AAAATTAGCA	5200
5201	AAGCTGATAA	TTGACTTATC	AGCAGGCGCT	GACATGACT	CTTCATATGC	CCTGCAAGAC	AGTGAAGCA	TTAATCAAGT	GCAGTGAGCA	TGGTCTCTGT	5300
5301	TTCAATTACTA	TAGAGGTTGA	TGAAATGATA	TGGACTCAA	AAGAATTAAA	AGAAGCTTTG	TCCGATGGGA	TAGTGAAGTC	TCACACCAAC	ATTTACAATT	5400
5401	GTTAATTAGA	AAACATAGAA	ATTATATATG	TCRAGGCTTA	CTTAAGTTAG	TAAAAACACA	TCAGAGTGGG	ATAAGTGACA	ATGATAACAT	TAGATGTCTAT	5500
5501	TAAAGTGTAT	GGGTCTTCAA	AAACATGTAC	TCACCTCAA	AAAATTATCA	AAGACCATTC	TGTAAGAGTG	CTTATTGTCG	TTAAGTTAAT	ATTAGCTTTA	5600
5601	CTAACAATTT	TCACAATAAC	AATCACTATA	AACTTACATA	AAAGTAGAAA	CAATCTACAA	ATATGCCACT	CAAAAACAGT	ATCAGACAAA	GAGACTCTAC	5700
5701	CATCAATATC	CACATCCGTC	ACAACCAAGA	CCACTCTAGA	CCATGATATA	ACACAGTATT	TTTAAAAGATT	AATTCAAAGG	TATACAGATT	TGTAATAATA	5800
5801	CAAGGACACA	TGCTGGAATA	TAAAGCAGAA	TCRATGCACA	AAATATAACA	CATATAAATT	TTTATGCTTT	AAACCTGAGG	ACTCAAAAT	CAACAGTTGT	5900
5901	GATAGACTGA	CAGATCTATG	CAGAAACAAA	TCAAAATCAG	CAGCTGAAGC	ATATCATACA	GTAGAATGCC	ATTGCATATA	CACAATTGAG	TGGAAGTGTG	6000
6001	ATCACCACTC	AATAGATTAA	ACCCAATCTT	GAATGTTAAA	ACTAGACTAG	GATCCGTCTA	AGACTATCAG	TTCAATAGTT	TAGTTATTTT	AAAATATTGG	6100
6101	AGAATFAGTA	AGTTTCTATG	GCACCTCATA	GCAATAGGTA	ATAATTAAACA	GCTTAATTAT	AATTAACAACA	TTATTTAAAA	TCGTAACAT	TTAATTTTACA	6200
6201	AGTAAAAAAC	AAAAATATGG	GACAAAGTAGT	TATGGAGGTG	AAAGTAGAGA	ACATTCCAGC	AATAGACATG	CTCAAAAGCAA	GAGTGAATAA	TGCTGTGGCA	6300
6301	CGTAGCAAT	GCTTTAAAAA	TGCTTCTTTA	ATCCTCATAG	GAATTAACATC	ACTGAGTATA	GCTCTCAATA	TCTATCTGAT	CATAAATAC	ACAATACCAA	6400
6401	AACTCTATC	TGAATCAGAA	CACCACACCA	GCTCACACC	CACAGRATCC	AACAAGGAAG	CTTCAACAAAT	CTCCACAGAC	AACCCAGACA	TCAATCCAAA	6500
6501	CTCACAGCAT	CCAACCTCAAC	AGTCCACAGA	AAACCCACA	CTCAACCCCG	CAGCATCAGT	GAGCCCATCA	GAACAGAAC	CAGCATCAAC	ACCAGACACA	6600
6601	ACAAACCGCC	TGTCCTCCGT	AGACAGGTCC	ACAGCACAA	CAAGTGAAGG	CAGAACAAG	ACAAAACCGA	CAGTCCACAC	AAGAAAACA	CCAAGCACAG	6700
6701	CTTCAGTAC	ACAATCCCA	CCACGGGCAA	CAACGAAGC	AATCCGAGA	GCCACCACTT	TCCGATGAG	CAGCACAGGA	AAAAGACCAA	CCACACATC	6800
6801	AGTCCAGTCC	GACAGCAGCA	CCACAACCCA	AAATCATGAA	GAACAGGTT	CAGCGAACCC	ACAGGCATCT	GTAGACACAA	TGCAAACTA	GCACACCAAC	6900
6901	AATATAAAAC	CAAAATTAGTT	AACAAAAAAT	ACGAGATAGC	TCTAAAGTAA	AACATGTAGG	TACCAACAAAT	CAAGAAACCA	AAAGACAAT	CACAATCTCC	7000
7001	CTAAACACGC	AACGACACCA	TGTGAGCTTT	GCTCAAAATCT	CTCTGGAGA	AACTTTTGCC	CACATCTAAA	CAACATCACA	ACCATCTCAA	GAAAAAGAAA	7100
7101	TGGGAAAAAC	AGCATCCAAG	AGACAAATAG	CAATGGATAG	TCTTAATGAA	TCCACTGTTA	ATGCTATCT	CCCTGATTCG	TACCTTAAAG	GAGTAATTTT	7200
7201	CTTTGAGTGA	ACTAATGCAA	TTGGTTTCATG	TCCTTTAAAA	AGACCTACT	TAAAAATGA	CACACTGCA	AAAGTTGCCA	TAGAGATCC	TGTTATTGAG	7300
7301	CATGTGAGAG	TCAAAATGTC	AGTCAATCT	AAAATGAAA	TATCAGATTA	CAAGTAGTA	GAGCCAGTAA	ATAGTCAACA	TGAAATAATG	AAAGATGTAC	7400
7401	ACAGTTGTGA	GCTCACACTA	TTGAAACAGT	TTTTAAACAAG	GAGTAAAAAC	ATTAGCACTC	TCAAAATTGAA	TATGATATGT	GATTGGCTGC	AATTAAGTAC	7500
7501	TACATCAGAT	GATACCTCAA	TCCTAAGTTT	CATAGATGTA	GAATTTATAC	CTAGTTGGGT	AAGCAACTGG	TTTAGTAATT	GGTACATCT	CAATAAGTTA	7600
7601	ATTTTGGAA	TCAGAGAGAG	GGAAGTAATA	AGAACCGGTT	CAATCTTATG	CAGGTCAATTG	GGTAAATTAG	TTTTTATTGT	ATCATCATAT	GGATGTATCG	7700
7701	TCAAGAGCAA	CAAAAGCAAA	AGAGTGAGCT	TCITCACATA	CAATCAACTG	TTAACATGGA	AAGATGTGAT	GTTAAGTAGA	TTTAATGCGA	ATTTTGTGAT	7800

Fig. 37B

HMPV strain 83 (continued)

7801 ATGGGTAAGC AATAGTCTGA ATGAAATATCA GGAAAGGCTA GGGTTGAGAA GTAAATCTGCA AGGTATGTTA ACTATAAAC TATATGAAAC TGTAGATTAT 7900
7901 ATGCTAAGCT TATGTTGCAA TGAAGGTTTC TCCTTTAGAT TCCTTAGGAT TACTGAACAT GCTCAATTCA 8000
8001 GTACTAAGTT TAGAAATACT TTATTGAATG GATTAAACAG TCAATTAAACA AATATTAATA ATGAAACACAG CATAGTACCG TATTAGAAA 8100
8101 TAATGATTAT CCAATGTATG AAGTTGTACT TAAATTATTA GGAGATACTT TGAGATGTAT CAAATTATTA ATCAATAAAA ACTTAGAGAA TGTGTCAGAA 8200
8201 TTATACTATA TATTAGAAAT TTTTGGTCAAT CCAATGGTAG ATGAAGAGAGA TGCAATGGAT GCTGTCAAAAT TAAACAATGA AATCAGAAA ATCTAAGGT 8300
8301 TGGAGAGCTT GACAGAACTA AGAGGGGCAT TCATATTAAG GATTATCAAA GGATTTGTGG ACAACAACAA AAGTGGCCC AAAATTAAAA ACTTAAAAAGT 8400
8401 GCTTAGCAAA AGATGGACTA TGTACTTCAA AGCTAAAAAT TACCCAGTGC AACTCGAATT AAGTGAACAA GACTTTCTAG AGCTTGTGTC AATACAAATT 8500
8501 GAACAAGAGT TTTCTGTCC TGAATAAAC AATCTTGAGA TGGTATTAAA TGACAAAAGCC ATATCACCTC CTAAAAGATT AATATGGTCT GTGTATCCAA 8600
8601 AGAATTACTT ACCTGAGACG ATAAAAAATC GATATTTAGA AGAACTTTC AATGCGAGTG ATAGTCTCAA AACAGAAAGA GTACTAGAT ACTATTAAA 8700
8701 AGATTAATAA TTTGTCAAA AGGAACCTTA AGTTATGTA GTTAGACAAG AATATTAAA CGATAAGGAG CACTTGTCT CATTAACTGG AAAAGAAAAGA 8800
8801 GAATTAAAGT TAGGTAGAA GTTTGCTATG CAACAGGAA AACAGCGACA AATACAAATA TTGGCAGAAA AATTGTTAGC TGATAACATT GTACCTTTCT 8900
8901 TCCCGGAAC CTTAACAAAG TATGGTGATC TAGATCTTCA GAGATAATG GAAATCAAAT CAGAACTTTC TTCTATCAA ACCAGAGAA GTAGTAGTTA 9000
9001 TAATAATTAC ATTGCAAGAG CATCCATAGT AACGATTG AGCAAGTTCA ACCAAGCCTT TAGATATGAA ACTACAGCGA TCTGTGCGA TGTAGCAGAC 9100
9101 GAATTACATG GAACACAAAG CTTATTCTGT TGGTTACATC TTATCGTTCC TATGACTACA ATGATATGTG CCTATAGACA TGCACCAACA GAAACAAAAG 9200
9201 GTGAATATGA TATAGATAAG ATAGAAGAGC AAGTGGTCT ATATAGATAT CACATGGGCG GTATTGAAGG ATGGTGTCAA AAACCTGGA CAATGGAAGC 9300
9301 TATATCTTTA TTGGATGTTG TATCTGTAAA GACACGGTGT CAAATGACAT CTTTATTAAA CGTGACAAAC CAATCAATAG ATGTAAGTAA ACCAGTCAAG 9400
9401 TTATCTGAAG GTTTAGATGA AGTGAAGGCA GATTATCGT TAGCAGTAAA AATGCTAAAA GAAATAAGAG ATGCATACAG AAATATAGGC CATAACTTAA 9500
9501 AAGAGGGCA AACATATATA TCAAGGGATC TTCAGTTTAT AAGCAAGGTG ATTCAATCTG AAGGAGTGT CACTCTACC CCTATAAAA AGCTTTTGAG 9600
9601 AGTAGAGCCA TGGATAACA CAATATTAGA TGACATTAAA ACTAGTCTG AGTCAATAGG GAGCTATGT CAAGAATTAG AATTAGGGG AGAAACATA 9700
9701 ATAGTTAGTC TGATATTAAAG AAACCTCTGG CTGTATAACT TATACATGCA TGAATCAAAG CAACATCCTT TGGCAGGGA ACAGTTATTG AAACAACATA 9800
9801 ATAAACATT AACATCAGTG CAGAGATTIT TTGAATTTAA AAGGAAAAAT GAGGTAGTAG ATCTATGGAT GAACATACCA ATGCAATTG GAGGAGGAGA 9900
9901 TCCAGTAGTC TTCTATAGAT CTTTCTATAG AAGGACCCCT GATTTTTAA CTGAGGCAAT CAGCCATGTA GATATTCTGT TAAAAATATC AGTAAACATA 10000
10001 AAAATGAAA CGAAAGTAAG TTTCTTCAA GCCTTACTAT CAATAGAAA AAATGAACGT GCTACACTGA CAACACTAAT GAGAGATCCT CAAGCTGTG 10100
10101 GATCAGAACG ACAAGCAAAA GTAACAAGTG ACATCAATAG AACAGCAGTT ACCAGTATCT TAAGTCTTTC CCCAAATCAA CTTTTCAGTG ATAGTGTAT 10200
10201 ACCTACAGC AGAAATGAAG AAGAAGTGGG AATCATGCA GAAACATAA CACCTGTTTA TCCTCATGGG CTGAGAGTAT TATATGAATC ATTGCCCTTT 10300
10301 CACAAAGCTG AAAAGTTGT AAACATGATA TCAGGACAA AATCTATAAC CCACTTATTA CAGAGAACAT CCGCTATTAA TGGTGAAGAT ATTGACAGGG 10400
10401 CTGTATCTAT GATGTTGGAG AATCTAGGAT TATTATCTAG AATATTGTC GTAGTTGTTG ATAGTATAGA AATTCCAATC AATCTAATG GTAGGTGAT 10500
10501 ATGTTGTCAA ATCTCTAGGA CTTTAAGAGA GACATCATGG AATAATATGG AAATAGTTGG AGTAAACATCT CCTAGCATCA CTACATGTAT GGTGTCTATA 10600
10601 TATGCAACTA GTTCTCATTT GAAAGGGATA ATTATAGAAA AGTTACAGAC TGACAGAACT ACAAGGGGTC AAAGAGGTCC AAAAGCCCT TGGGTAGGT 10700
10701 CGAGTACTCA AGAGAAAAA TTAGTACCTG TTTATAACAG ACAATCTC TCATAAACAC AAAGAGAAC GCTAGAACGA ATTGAAAAA TGAGATGGT 10800
10801 GTATAAAGG ACACAGGCT TGGGACGATT ACTCAACAAG ATCTGTCTTG GGAGTTTAGG CATTAGCTAC AAATGTGTAA AACCTTATT ACCTAGTTT 10900
10901 ATGAGGTAA ATTTCTTACA TAGATTATCT GTCAGTAGTA GACCTATGGA ATTCCAGCA TCAGTTCCAG CTTTATAGAAC AACAATTAC CATTCGACA 11000
11001 CTAGTCCCTAT TAATCAAGCA CTAAGTGAGA GATTTGGGAA TGAAGATATT AACTTGTCT TCCAAAAATGC AATCAGCTGT GGAATTAGCA TAATGAGTGT 11100
11101 AATTAGACAA TTAACAGGTA GAAGCCCAA ACAGTTAGT TTAATACCCC AATTGAAGA ATPAGACATT ATGCCACCAC CAGTGTTC AAGGAAATTC 11200
11201 AGTTATAAAT TAGTAGATAA GATACTTCT ATCAACATA TCTTTAGTCC GGACAAAATA GATTGTGTTA CATTAGGACA GCATTGACAT CCCACTATA 11300
11301 AAGGTCAGAA AACAGATCAG TTCTTAAATA AGACAGAAA TTATTCCAT GGAAACAAATC TTATTGAGTC TTTATCGGCA GATCATGCTT CCAATATTC 11400
11401 TGGGATATTA ACAGACAAT GCATAGAAA TAATATTTTC AAGAAGACT GGGGTGACGG GTTTATATCA GATCATGCTT TTATGGACTT CAAAATATTC 11500
11501 CTATGTGTCT TTAATACTAA ACTTTTATGT AGTTGGGGAT CTCAGGGGAA AAACATTAAA GATGAAGATA TAGTAGATGA ATCAATAGAT AAATTTGTTA 11600
11601 GGATTGACAA TACTTTTGG AGAATGTTCA GCAAGTTAT GTTTGAACTA AAGGTTAAGA AAAGGATAT GTTATATGAT GTAAATTC TATCACTAGT 11700
11701 AGGCTACATA GGGTTTAAAGA ACTGGTTTAT AGACAGTTG AGATCAGCTG AATTGCAATG AATACCTTGG ATTGTCAATG CCGAAGGTGA TTTGGTTGAG 11800

Fig. 37C

HMPV strain 83 (continued)

11801	ATCAAGTCAA	TTAAATCTA	TTTGCAACTG	ATAGAACAAA	GCTTATTTTT	AAGAATAAAT	GTTTTGAAC	ATACAGATAT	GGCACATGCT	CTCACACGAT	11900
11901	TAATCAGAAA	GAAGTTAATG	TGTGATAATG	CACGTGTTAA	CCCAATTTC	TCCCCAATGG	TTAACTTAA	TCAAGTTATT	GATCCCAAA	CACAATTAGA	12000
12001	TTACTTCCCC	AAGATAACAT	TCGAAAGGCT	AAAAAATTAT	GACACAAGTT	CAAAATTATGC	TAAAGGGAAG	CTAACAGAA	ATTACATGAT	ACTATTGCCA	12100
12101	TGGCAGCATG	TTAATAGATA	TAACTTTTGC	TTTAGTTCTA	CTGGATGTAA	AGTTAGTCTG	AAAACATGTA	TTGGAAAACT	TATGAAAGAC	CTAAATCCTA	12200
12201	AAGTTTGTGA	CTTTATTGGA	GAAGGAGCAG	GAAATTGGAT	GGCCAGAACAA	GCATGTGAAT	ATCCTGATAT	TAAATTGTGA	TATAGAAGTC	TGAAAGATGA	12300
12301	CCTTGATCAT	CATTATCCTC	TGGAATACCA	GAGATGATA	GGTGAATTAA	GCAGAAATCAT	AGATAGTGGT	GAAGCACTTT	CAATGGAAC	AACAGACGCA	12400
12401	ACTCAAAAAA	CTCATTGGGA	TTTGATACAC	AGGGTAAGCA	AAGATGCTTT	ATTAATAAAT	TTATGTGATG	CAGAATTAA	GGACAGAGAT	GATTTTTTTA	12500
12501	AGATGGTAAT	TCTATGGAGA	AAACATGTAT	TATCATGCAG	AATTTGCAC	ACTTATGGGA	CGGACCTCTA	TTTTATTGCA	AAGTATCATG	CTAAAGACTG	12600
12601	CAATGTAAAA	TTACCTTTTT	TTGTGAGATC	AGTTGCTACT	TTTCAATTATGC	AGGGTAGTAA	GCTGTCAAGT	TCAGAAATGCT	ACATACTCTT	AACACTAGGC	12700
12701	CACCACAACA	GTTTACCTTG	CCATGGAGAA	ATACAAAATT	CTAAGATGAA	AATAGCAGTG	TGTAATGATT	TTTATGCTGC	AAAAAACTC	GACAATAAAT	12800
12801	CAATTGAAGC	TAATTGTAAA	TCACCTTTTGT	CAGGCTAAG	AATACCTATA	AATAAGAAGG	AACTAGATAG	ACAGAGAAGA	TTATTACAC	TACAAAGCAA	12900
12901	TCATTCTTCT	GTAGCAACAG	TTGGCGGTAG	CAAGATCATA	GAGTCTAAGT	GGTTAACAAA	CAAAGCAAGT	ACAATAATTG	ATTGGTTAGA	ACATATTTTA	13000
13001	AATTCTCCAA	AGGGCGAATT	AAATTATGAT	TTTTTTGAAG	CATTGGAGAA	CACCTTACCCT	AAATGATTTA	AACTAATAGA	TAACTTAGGG	AATGCAGAGA	13100
13101	TTAAAAAAT	GATCAAGTA	ACAGGATACA	TGCTTGTAAG	TAAAAATGA	AAAATGATGA	AGATGACAAA	ATAGATGACA	ACTTCATACT	ATTCTAAATT	13200
13201	AATTATTGTA	TTATGCAATT	ATATGATAGT	TAATTAAAT	TAAAAATTAA	AAATCAAAAAG	TTAAAAATTTA	AAACCTATCA	TTAAGTTTAT	TAAAAATAAG	13300
13301	AAATTATAAT	TGAATGTATA	CGGTTTTTTT	GCCGT							13335
	10	20	30	40	50	60	70	80	90	100	

Fig. 37D

rHMPV-GFP

	10	20	30	40	50	60	70	80	90	100
1	ACGCGAAAAA	AACGCGTATA	AATTAAGTTA	CAAAAAAACA	TGGGACAAGT	GAAATGTGTG	AGCAAGGGCG	AGGAGCTGTT	CACCGGGGTG	GTGCCCATCC
101	TGGTGTAGCT	GGACGGGCAC	GTAACCGGC	ACAAGTTTCA	CGTGTCCGGC	GAGGCGGAGG	GCAGTGGCCG	CTAGCCCTGA	AGTTTCATCTG	200
201	CACACCGGGC	AAGCTGCCCC	TGCCCTGGCC	CACCTTCGTG	ACCACCTTGA	CCTACGGCGT	GCAGTGGCTC	AGCGGTACC	CGACACATC	GAAGCAGCAC
301	GACTTCTTCA	AGTCCGCCAT	GCCCGAAGGC	TACGTCCAGG	AGCGCACCAT	CTTCTTCAAG	GACGACGGCA	ACTACAAGC	CCGCGCCGAG	GTGAAGTTCTG
401	AGGGCGACAC	CCTGTGTGAC	CGCATCGAGC	TGAAGGGCAT	CGACTTCAAG	GAGGACGGCA	ACATCCTGGG	GCACAAGCTG	GAGTACAACT	ACAACAGCCA
501	CAACGTCTAT	ATCATGTGGC	ACAGCAGAA	GAACGGCATC	AAGTGAAT	TCAAGATCCG	CCACAACATC	GAGGACGGCA	CGGTGCAGCT	CGCGGACCCAC
601	TACCAACAGA	ACACCCCAT	CGCGGACGGC	CCCGTGTCTG	TGCCCGACAA	CCACTACTCTG	AGCACCCCAT	CCGCGCTGAG	CAAGAGCCCC	AACGAGAAGC
701	CGCATACACAT	GGTCTGTCTG	GAGTTCGTGA	CCGCGCGCCG	GATCACTCTC	GGCATGAGC	AGCTGTACAA	GTAAGTTAAT	TAAAAAAGTG	GGACAAGTGA
801	AAATGTCTCT	TCAAGGGATT	CACCTGAGTG	ATCTATCATA	CAAGCATGCT	ATATTAAAG	AGTCTCAGTA	TACATAAAG	AGAGATGTAG	GCACAACAAC
901	AGCAGTGACA	CCCTCATCAT	TGCAACAAGA	AATACACTA	TTGTGTGGAG	AAATTTCTATA	TGCTAAGCAT	GCTGATTACA	AATATGCTGC	AGAAATAGGA
1001	ATACATATA	TTAGCAGAGC	TCTAGGATCA	GAGAGAGTAC	AGCAGATTCT	AAGAACTCA	GGCAGTGAAG	TCCAAGTGGT	TTTAACCGA	AGTACTCTCT
1101	TGGGGAAGT	TAAAAACAAC	AAAGGAGAAG	ATTTACAGAT	GTTAGACATA	CACGGAGTAG	AGAAAAGCTG	GGTGAAGAG	ATAGACAAAG	AGCAAGAAA
1201	AACAAATGGCA	ACTTTGCTTA	AAGAATCATC	AGGCAATATT	CCACAAAATC	AGTCAGAGA	GCTAACCCGTG	TACTAAGTGA	TGCACCTCAA	AGATACCCCTA
1301	TTAATATTTA	CCAACTAGC	ATCAACTATA	GAAGTGGGAT	TAGAGACCCAC	AAAGTGTATT	ACAGAAAGTTT	GTTCAATTGAG	TATGGCAAG	CATTAGGCTC
1401	GGATGGACAT	ACCAAAAATC	GCTAGATCTT	TCTATGATTT	ATTTGACAAA	AAAGCTTACGG	TGCTGGTCAA	ACAATGCTGA	GGTGGGAGT	CATTGCCAGG
1501	ATCCTCTACA	GGCAGCAAAG	CAGAAAGTTT	ATTCGTTAAT	ATATTCTATC	AAGCTTACCA	GAAGTCTATG	ACCTGGTGGC	AGAAATGGGC	CCTGAATCTG
1601	TCATCTAACA	ATATAATGTT	AGGACATGTA	TCTGTCCAAG	CTGAGTTAAA	AATTGTCCCA	ACTTTGCAAG	TGTTTCTCTC	GGCAATGCCT	CAGGCTTAGG
1701	GCTCTCTAGA	TTTAAGGCAA	AGCCCAAAAG	CTGAGCTGTT	ATCATTTAGC	CAGCAGAAAG	CTATGCCCAA	AGTTTGAAG	AGAACTATA	AATTAACCTT
1801	CATAATAGAT	ATGATCGCG	GGAGAGTGCC	AAACACAGAA	CTATTTTTCG	AAATGTGAGT	GACGACAGTC	AAAATGATTA	TGAGTAATTA	AAAAAGTGGG
1901	TCTTCATTAG	GACTCAGACA	TGAAGAAAAA	GAGGCTGCAG	AACACTTTCT	ATGAAGGGGC	AAAATTGGCA	GAAGCTTTCC	AAAAATCATT	AAGAAAACCT
2001	ACAACTCAAA	ATGTCTATCC	CTGAAGGAAA	AGATATTCTT	TTTATGGGTA	TGAACACTTG	GAATTACCTA	CTATCAGTAG	ACCTACCAA	CCGACCATAT
2101	AGTCAATAAA	GATCTCAATC	TATTATAGGA	GAATAAGTGA	ACACTGTATC	GAAGCAAAAGC	AAACAATCAA	AGTTATGGAT	CCTATTGAAG	AAGAAGAGTT
2201	TGTCAGAGCC	GAAGTTAGCA	TGGACAGACA	AAAGTGGGGC	AATCAAAACT	AGAAAGTTGAA	ACCATCAACC	AATACTAAA	AGAAGTCTC	ATTTACACCA
2301	TACTGAGAAA	AGGGTGTCTG	CCTCCAGTGA	TGGGAAAAC	CCTGCAGAAA	TTTCAACAAT	GAAGAAGAAG	ATGCAGAAATC	CTCAATCTTA	ACCTTCGAAG
2401	AATGAACCCAG	GAATAATACAC	AAAGTTGGAG	AAAGATGCTC	TAGACTTGCT	GAGAAATTA	GCATGATATT	AGGGCTATTA	AGAACACTCA	ACATTTGCTAC
2501	AAAGAGATAC	TTCATCATTA	AGCATTTGAAG	CCAGACTAGA	ATCGATTGAG	TAAAGGAGGA	ACTAATAGCA	GACATAATA	AAGAAGCAA	GGGAAAAGCA
2601	AGCAGGACCC	ACAGCAGCAA	GAGATGGGAT	CAGAGATGCA	ATGATTGGCA	TAGTGTAAA	TTAACTGAAA	AGGCAAGGA	GCTCAACAA	ATTGTTGAAG
2701	GCAGAAATGA	TGGAAGAAGA	AATGAACCCAG	CGGACAAAAA	TAGGAAACGG	CAGGAAAATA	ATCAAGAAGA	TGACATTTAC	CAGTTAATTA	TGTAGTTTAA
2801	ACGAGAGCAC	AAGTGTGTGA	TCCGAAGAAG	AAGAAGAACT	AAAAGACACA	CTATCAAGGC	ATCCCTTACA	CAGCAGCTGT	TCAAGTTGAT	CTAGTAGAAA
2901	TAAAAATAAA	AAATGGGACA	AGTGAAAATG	GAGTCTTATC	TGTTAGACAC	AATACACAC	CAGCAGTTCT	GCTTGATCAG	CTAAAGACTC	TGACTATTAAC
3001	AGGACTGTGT	ACCTGCAAGC	CTAACAAAT	GGTTCCCCCT	GTTTCAGGCC	CGGCCCAAGG	TGCAGCAATG	TCTGTACTTC	CCAAAAGTT	TGAAGTCAAT
3101	TACTCTGTAT	GCTGCATCAC	AAAGTGTCTC	AATACTAAA	GTGAATGCAT	AGTCTGTGAA	GTAATAACAG	TTTTACTTAAC	AACCATGAAA	CCATATGGGA
3201	CGGACTGTAG	CACCTTGACGA	ATATAGCAAA	TTGAATTTG	ACAACTTAC	GATCTAATCG	CATTATGCGA	TTTTATGGAT	CTAGAAAAGA	ACACACCACT
3301	TGATATCAAA	GTTTGTGAGC	TGCGCCAAAC	CAGTTGGCAA	AAAAACACAT	CCACTGTGGA	AGGTGCAATA	AGCTTGAGG	TGAGCAAGC	TCTAACACAA
3401	TACCAATACA	GCTTTTATCA	AATCAGTTTC	TATCAAGGAG	AGTGAATCAG	TCCCAAGGC	ATATTCAATA	AGCTTGGAG	TGGACCCAA	TGTATAGTAG
3501	GCCAAAATTG	CACCTTATGC	GGGACTGATC	ATGATTATGA	CCATGAACAA	TGGAGCCATC	AAGGAACAAAG	ATATGTGCTG	AAGTCCAGAT	AACAGCCAAAG
3601	AACTAGGAGC	ATATGTCCAG	GCTGAAGACA	TAACTAAAAT	ATGCAAGACT	TTTTAGTTAT	ATAAAAATCA	AGTTAGAATA	AGATGCTAG	CAATCAAGAA
3701	CAACTGACC	AAGAACTACC	AACTCTATTC	TATAGACTAA	AAAGTCGCCA					

Fig. 38A

rHMPV-GFP (continued)

3801 CGGACAAAT AAAAATGTCT TGGAAAGTGG TGATCAATTT TTCAATTGCTA ATAACACCTC AACACGGTCT TAAAGAGAGC TACCTAGAAG AATCATGTAG 3900
3901 CACTATAACT GAGGATATC TTAGTGTCTT GAGGACAGGT TGGTATACCA AGGTTTTTAC ATTAGAGGTG GGTATGTAG AAAACCTTAC ATGTTCTGAT 4000
4001 GGACCTAGCC TAATAAAAC AGAATTAGAT CTGACCAAAA GTGCACATAAG AGAGTCTCAA ACAGTCTCTG CTGACCAATT GGCAAGAGAG GAACAAATTTG 4100
4101 AGAATCCCGAG ACAATCTAGG TTTGTTCTAG GAGCAATAGC ACTCGGTGTT GCAACAGCAG CTGCAGTCAC AGCAGGTGTT GCAATTTGCC AAACCATCCG 4200
4201 GCTTGAGAGT GAAGTCACAG CAATTAAGAA TGCCCTCAAA ACAGACCAATG AAGCAGTATC TACATTTGGG AATGGAGTTC GAGTGTGGC AACTGCAGTG 4300
4301 AGAGAGCTGA AAGACTTTGT GAGCAAGAA TTAACCTCGT CAATCAACAA AAACAAGTGC GACATTTGAT ACCTAAAAAT GGCCGTTAGC TTCAGTCAAT 4400
4401 TCAACAGAAG GTTCTTAAT GTTGTGCGG AATTTTCAGA CAATGCTGGA ATAACACACG CAATATCTTT GGACTTAATG ACAGATGCTG AACTAGCCAG 4500
4501 GGCCGTTCT AACATGCCG CATCTGCAG ACAATAAAA TTGATGTGG AGAACCGTGC GATGTTGCGA AGAAGGGGT TCGGAATCCT GATAGGGGTC 4600
4601 TACGGGAGCT CCGTAATTA CATGGTGCAG CTGCCAATTT TTGGCGTTAT AGACACGGCT TGCTGGATAG TAAAGACAGC CCCTCTTGT TCCGGAAAAA 4700
4701 AGGGAACCTA TGCTTGCCCT TTAAGAGAG ACCAAGGGT GTATTGTCAG AATGACGGT CAATGTTTTA CTACCCAAAT GAGCAAACT 4800
4801 AGGAGACCAT GTCTTTTGGG ACACAGCAG GGGAAATTAAT GTTTGTCAG AATCAAGGA GTGCAACATC ACATATCCA CCAAAATTA CCAATGCAAA 4900
4901 GTCAGACAG GAAGACATCC TATCAGTATG GTTGCACTGT CTCCTCTTGG GGCTCTGGTT GCTTGCTACA AAGAGTAAG CTGTTCCATT GGCAAGCAAA 5000
5001 GAGTAGGGT CATCAAGCAG CTGAACAAGG GTTGCTCTTA TATAACCAAC CAAGATGCAG ACACAGTGAC AATAGACAACT ACTGTATATC AGCTAAGCAA 5100
5101 AGTTGAGGGT GAACAGCATG TTATAAAGG CAGACCATG TCAAGCAGCT TTGATCCAAAT CAAGTTTCCCT GAAGTCAAT TCAATGTTGC ACTTGACCAA 5200
5201 GTTTTGTAGA ACATTTGAAA CAGCCAGGCC TTGTAGATC AATCAACAG AATCTTAAGC AGTGCAGAGA AAGGAATATC TGGCTTCATC ATTGTAATA 5300
5301 TTTCAATTGC TGTCCTTGGC TCTAGCATGA TCCTAGTGAG CATCTTCATT ATAATCAAGA AAACAAGAA ACCAACGGGA GCACCTCCAG AGCTGAGTGG 5400
5401 TGTCACAACT AATGGCTTCA TACCACACAG TTAGTAAAT AAAAATAAAA TAAATTTGG GACAAATCAT AATGCTCGC AAGGCTCCAT GCAAAATATGA 5500
5501 AGTGGGGG AATGCAAC GAGGAAGTGA GTGTAAATTT AACCAATTT ACTGGAGTG GCAGATAGA TACTTATTA TTAATATAA TTAGTCAAA 5600
5601 ATCAGACTTT TAAGGAACAC TGATAGAGCT GATGGCTAT CAATAATAT AGGCGCAGG ACAGGAAGCA CAATCAAG CAATCAAG AAGTTGAAT 5700
5701 ATGTGTTTCA AGTTTATTT GATGATAAC AAAGCTGCA GCCTGTACA GTCTACACAA CATATCAAG CAATCAAG CCAACTCC CGCATCTTTA 5800
5801 TAGGACGGT AGATATGCA AACTATCTGA CAGCAAGCAT GTGGACTCC AATACTTAAT CTATCTTAC ATGAGATGA GCAAACTCC CGCATCTTTA 5900
5901 ATCAACAATC TCAAAAGACT GCGGAGAGAA AAATGAAA AATTAGCAA GCTGATAAT GACTTATCAG CAGGCGCTGA CAATGACTCT TCATATGCC 6000
6001 TGCAAGACAG TGAAGCATT AATCAAGTGC AGTGAGCATG GTCTCTTTT CATTACTATA GAGTTGATG AATGATATG GACTCAAAA GAATTAAG 6100
6101 AAGCTTTGTC CGATGGGATA GTGAAGTCTC ACACCAACAT TTACAATTGT TATTTAGAAA ACATAGAAAT TATATATGTC AAGCTTACT TAAGTTAGTA 6200
6201 AAACACATC AGATGGGAT AAGTGACAA TATGACATT GATGTCATTA AAAGTGATGG GTCTCAAAA ACATGTACTC ACCTCAAAA AATAATCAA 6300
6301 GACCATTTG GTAAAGTGT TATTGCACTT AAGTTAATAT TAGCTTTACT AACATTTTC ACAATAACAA TCATATAAA TTACATAAAA GTPAGAAAAA 6400
6401 ATCTACAAAT ATGCCAGTCA AAAACTGAAAT CAGACAAAGA AGACTCACCA TCAAAATACCA CATCCGTAC ACCAAGACC ACTCTAGACC ATGATATAAC 6500
6501 ACAGTATTTT AAAAGATTAA TTCAAAGGTA TACAGATTCT GTAATAAACA AGGACACATG CTGGAATAA AGCAGAAATC AATGCACAA TATAACAA 6600
6601 TATAAATTTT TATGCTTTAA ACCTGAGGAC TCAAAAATCA ACAGTTGTGA TAGACTGACA GATCTATGCA GAAACAAATC AAAATCAGCA GCTGAAGCAT 6700
6701 ATCATACAGT AGAATGCCAT TGCATATACA CAATTGAGTG GAAGTGCTAT CACCCTCAA TAGATTAAAC CCAATCTTGA ATGTTAAAC TAGACTAGGA 6800
6801 TCCGCTAAG ACTATCAGTT CAATAGTTTA GTTATTTTAA AATATTGAG AATAGGTAAG TTTCTATGGC ACTCATAGC AATAGGTAAT AATTAACAGC 6900
6901 TTAATTATAA TTAACAATTT ATTAAATC GTAACTATTT AATTACAAA GTAAAAACAA AAATATGGGA CAAGTAGTTA TGGAGGTGA AGTAGAAG 7000
7001 ATTCGAGCAA TAGACATGCT CAAGCAAGA GTGAAAAATC GTGTGCGACG TAGCAATGC TTTAAAAATG CTTCTTTAAT CCTCATAGGA ATAACATAC 7100
7101 TGAGTATAGC TCTCAATATC TATCTGATCA TAACTACAT AATCAAAA ACCTCATCTG AACTCAACAG TCCACAGGAG CCACACCCA CAGAAATCAA 7200
7201 CAAGTAGTGA GCGCATCTC TCAACAATCT CCACAGACAA GCATCAACAC CACAGACATC CACAGATCC AACTCAACAG TCCACAGGAA ACCCACACT CAACCCCGA 7300
7301 GCATCAGTGA GCGCATCTC TCAACAATCT CCACAGACAA GCATCAACAC CACAGACATC CACAGATCC AACTCAACAG TCCACAGGAG ACACACCA 7400
7401 GAACAAAGAC AAAACCGACA GTCCACACAA GAACAACCC AAGCAGACT TCCAGTACAC AATCCCAAC ACAGGCAACA ACAGGAGCAA TCCGAGAGC 7500
7501 CACCACTTTC GCGATGAGCA GCACAGGAAA AAGACCAACC ACAACATCAG TCCAGTCCGA CAGCAGACAC ACAACCCAAA ATCATGAAGA AACAGGTTCA 7600
7601 GCGAAGCCAC AGGCATCTGT AAGCAATATG CAAACTAGC ACACCAACA TATAAACCA AATTAGTTAA CAAAAATATC GAGATAGCTC TAAAGTAAAA 7700
7701 CATGTAGGTA CCAACAATCA AGAAACCAAA AGAACAATCA CAATCTCCCT AAAACAGCAA CGACACCATG TCAGCTTTGC TCAATCTCT CTGGGAGAAA 7800

Fig. 38B

rHMPV-GFP (continued)

7801 CTTTGGCCCA CATACTAACA ACATCAACAAC CATCTCAAGA AAAGAAACTG
7901 CACTGTAAAT GTCTATCTCC CTGATTCGTA CCTTAAAGGA GTAAATTTCTT
8001 AAAAATGACA ACACTGCAAA AGTTGCCATA GAGAACTCTG TTATTGGAC
8101 AGGTAGTAGA GCCAGTAAAC ATGCAACATG AAATAAATGAA GAATGTACAC
8201 TAGCACTCTC AAATTGAATA TGATATGTGA TTGGCTGCAA TTAAAGTCTA
8301 AGTTGGGTAA GCAACTGGTT TAGTAATTGG TACAACTCTCA ATAAGTTAAT
8401 GGTCATTTGG TAAATTAGTT TTATTGTAT CATCATATGG ATGTATCGTC
8501 AACATGGAAA GATGTGATGT TAAGTAGATT TAATGCGAAT TTTTGTATAT
8601 AATCTGCAAG GTATGTTAAC TAATAAACTA TATGAAACTG TAGATTATAT
8701 GTTTTATTAT GAGTGAGATC CTTAGGATTA TAGTACCGTA TTAGAAAATA
8801 ATTTAAATAT AAAAACAGAC TCAGAGTTCA TAGTACCGTA TTAGAAAATA
8901 AGATGTATCA AATTATTAAT CAATAAAAC TTAGAGAAATG CTGCAGAAAT
9001 CAATGGATGC TGTCAAATTA AACAAATGAA TCACAAAAT CCTAAGGTTG
9101 ATTTGTGGAC AACAAACAAA GGTGGCCCAA AATTAAAAAC TTAAAGTGC
9201 CTCGAATTAA GTGAACRAGA CTTTCTAGAG CTTTCTGCAA TACAATTGA
9301 ACRAAGCCAT ATCACCCTCT AAAAGATTAA TATGCTCTGT GTATCCAAAG
9401 TGCAGGTAT AGTCTCAAAA CAAGAAGAGT ACTAGAGTAC TATTTAAAGG
9501 TTTTAAACG ATAAGGACA CATTGTCTCA TTAATGGAA AAGAAGAGA
9601 TACAAATATT GGCAGAAAA TTGTTAGCTG ATACATTTGT ACCTTTCTTC
9701 AATCAAAATCA GAACTTTCTT CTATCAAAAC CAGAAGAAAT GATAGTTATA
9801 CAAGCCTTTA GATATGAAC TACAGCGATC TGTGGGATG TAGCAGACGA
9901 TGACTACAAT GATATGTGCC TATAGACATG CACCACCAGA AACAAAGGT
10001 CATGGCGGT ATTGAAGAT GTGTCAACCA ATCAATAGAT GTAGTAAAC CAGTCAAGTT
10101 TTATTAACG GTGACAACCA ATCAATAGAT GTAGTAAAC CAGTCAAGTT
10201 TGCTAAAGA AATAAGAT GCATACAGAA ATATPAGGCA TAACTTAA
10301 TCAATCTGAA GGAGTATGC ATCCTACCCC TATAAAAAAG GTCTTGAGAG
10401 TCAATPAGGA GTCTATGTCA AGAATTAGAA TTTAGGGGAG AAAGCATAAT
10501 AATCAAAAGCA ACATCCTTTG GCAGGGAAC AGTTATTCAA ACAACTAAAT
10601 GGTAGTAGAT CTATGGATGA ACATACCAAT GCAATTTGGA GGAGGAGATC
10701 GAGCAATCA GCCATGTAGA TATTTCTGTA AAAATATCAG CTAACATAAA
10801 ATGAACGTGC TACACTGACA ACATAATGA GAGATCCTCA AGCTGTTGGA
10901 CAGTATCTTA AGTCTTTCCC CAAATCAACT TTTTCAGTGT AGTGCTATAC
11001 CTTGTTATC CTATGGGCT GAGAGATTTA TATGAATCAT TGCCCTTTCA
11101 ACTTATTACA GAGACATCC GCTATTATG TGAAGATAT TGACGGGCT
11201 AGTTGTTGAG TAACATCTCC TAGCATCTCA ATCTAATGGT AGCTGATAT
11301 ATAGTTGGAG TAACATCTCC TAGCATCTCA ATCTAATGGT AGCTGATAT
11401 ACAGAACTAC AAGGGTCAA AGAGGTCAA AAGGCCCTTG GGTAGGCTG
11501 AAAACAACAA AGAGACAGC TAGAAGCAAT TGGAAAAATG AGATGGGTGT
11601 AGTTTAGGCA TTAGCTACAA ATGTGTAAAC CCTTTATTAC CTAGGTTTAT
11701 TCCAGCATC AGTTCCAGCT TATAGAACAA CAAATTACCA TTTCGACAT

GGCAAAACAG CATCCAAGAG ACAATATAGCA ATGGATCCTC TTAATGAATC 7900
TTAGTGAAC TAATGCAAT GGTTCATGC TCTTAAAAAG ACCCTACTTA 8000
TGTGAGACTC AAAATGCGAG TCAATCTTAA AATGAAATA TCAGATTACA 8100
AGTTGTGAGC TCACACTATT GAAACAGTTT TTAACAAGGA GTAAAAACAT 8200
CATCAGATGA TACCTCAATC CTAAGTTTCA TAGATGTAGA ATTATACCT 8300
TTTGGAAATC AGAAGAGAGG AAGTAATAAG AACCGTTCA ATCTTATGCA 8400
AAGAGCAACA AAGCAAAAAG AGTGACTTC TTCACATACA ATCAACTGTT 8500
GGGTAAGCAA TAGTCTGAAT GAAATCAGG AAGGCTAGG GTTGAGAAGT 8600
GCTAAGCTTA TGTGCAATG AAGGTTCTC ACTTGTAAA GAGTTCGAAG 8700
ACTAGATTTA GAAATACTTT ATTGAATGGA TTAACAGATC AATTAACAAA 8800
ATGATTTACC AATGTATGAA GTTGTACTTA AATTATAGG AGATACTTTG 8900
ATACTATATA TTCAGAAATTT TTGTCATCC AATGTAGAT GAAAGAGATG 9000
GAGAGCTTGA CAGAACTAAG AGGGCATTC ATATTAGGA TTATCAAAAG 9100
TTAGCAAAAAG ATGACTATG TACTTCAAAG CTAAAATTA CCCAGTCAA 9200
ACAAAGTTT TCTGTTCTG AAAAAACCA TCTTGAGATG GTATTAAATG 9300
AATTACTTAC CTGAGACGAT AAAAAATCGA TATTTAGAG AACCTTTCAA 9400
ATAATAAAT TGATCAAAAG GAACTTAAA GTTATGTAGT TAGCAAGAA 9500
ATTAAGTGA TTGATAATGT TTGTATGCTA ACCAGAAA GACGACAAA 9600
CCGAAACCT TTAACAAAGT TGGTATGCTA GATCTTCAA GAAATATGGA 9700
ATAATTACAT TGCAAGAGCA TCCATAGTAA CAGATTTGAG CAACTTCAAC 9800
ATTACATGGA ACACAAAGT TATTTCTGTT GTTACATCTT ATCGTTCTTA 9900
GAATATGATA TAGATAAGAT AGAAGAGCAA AGTGTCTAT ATAGATATCA 10000
TATCTTTAT GATGTTGTA TCTGTAAAG CACGGTGTCA AATGACATCT 10100
ATCTGAAGT TTAGATGAAG TGAAGGCAGA TTATCGTTA GCAGTAAAAA 10200
GAAAGGAAA CATATATATC AAGGATCTT CAGTTTATAA GCAAGGTGAT 10300
TAGGACCATG GATAAACACA ATATTAGAT ACATTAACAC TAGTGTGAG 10400
AGTTAGCTG ATATTAGAA ACTTCTGGCT GTATACTTA TACATGCATG 10500
AAAACATTA CATCAGTGCA GAGATTTTT GAAATTTAAA GGGAAATGA 10600
CAGTAGCTT CTATAGATCT TTCTATAGAA GGACCCTGA TTTTAACT 10700
AAATGAACG AAGTAAAT TCTTCAAAG CTTACTATCA ATAGAAAAA 10800
TCAGAACGAC AAGCAAAAGT AACAGTGAC ATCAATAGAA CAGCAGTTAC 10900
ACTACAGCAG AATGAAGAA GAAGTGGAA TCATTGCGA AACATAACA 11000
CAAGCTGAA AAGTTGTAA ACATGATATC AGGACAAAA TCTATAACA 11100
GTATCTATGA TGTGGAGAA TTAGGATTA TATCTAGAA TATGTCACT 11200
TTTCTAAT CTCTAGGAT TTAAGAGAA CATATGGA TAATATGGA 11300
TGCAACTAGT TCTCATTTGA AAGGATAAT TATAGAAAAG TCAGCAGCTG 11400
AGTACTCAAG AGAAAAAT AGTACTGTT TATAACAGC AATTTCTCTC 11500
ATAAAGGAC ACCAGGCTG CGACGATTAC TCAACAGAT CTGTCTTGG 11600
GAGTGAAT TTTCTACATA GATTATCTGT CAGTAGAGA CCTATGGAAT 11700
AGTCTTATTA ATCAAGCACT AAGTGAGAGA TTTGGGAATG AAGATATTA 11800

Fig. 38C

HMPV strain 75

	10	20	30	40	50	60	70	80	90	100
1	ACGCGAAAA	AACGCGTATA	AATTAATTC	CAAAACAAA	GGGCAAAATA	AAAATGTCTC	TTCAAGGGAT	TCACCTAAGT	GATCTGTCA	ATAAACATGC
101	TATATTAAAA	GAGTCTCAAT	ACACAATAAA	AAGAGATGTA	GGCACCACAA	CTGCACTGAC	ACCTTCATCA	TTGCAAGCAG	AGATAACAT	TTTGTGTGGA
201	GAGATTCTTT	ACACTAAACA	TACTGATTAC	AAATATGCTG	CAGAGATAGG	GATACAATAT	ATTGTCACCG	CTCTAGGATG	AGAAAGAGTA	CAACAGATT
301	TAAGAAATTC	AGGCAGTGAA	GTTCAAGGTG	TTCTAACCAA	GACATACCT	TTAGGGAAAG	GTAAGAAATAG	TAAAGGGGAA	GAGTTGCAAA	TGTTAGATAT
401	ACATGAGGTG	GAAAAGAGTT	GGGTAGAAGA	AATAGACAAA	GAGGCAAGAA	AAACAATGGT	GACTTTGCTA	AAGGAATCAT	CAGGTAACAT	CCACAAAAAC
501	CAGAGGCTTT	CAGCACCAGA	CACACCAATA	ATTTTATTAT	GTGTAGGTGC	TTTAATATTC	ACTAAACTAG	CATCAACAAT	AGAAAGTTGA	CTAGAGACTA
601	CAGTTAGAAG	AGCTAACAGA	GTGCTAAGTG	ATGCGCTCAA	AAGATACCT	AGGGTAGATA	TACCGAAGAT	TGCTAGATCT	TTCTATGAAC	TATTTGAGCA
701	GAAAGTGAT	TACAGGAGTC	TATTCATTGA	GTATGGGAAA	GCTTTAGGCT	CATCTTCAAC	AGGAAGCAAA	GCAGAAAGTT	TGTTTGTA	TATATTTATG
801	CAAGCTTATG	GAGCCGGTCA	AACAATGCTA	AGGTGGGGTG	TCATTGCCAG	ATCATTTAAC	AACATAATGC	TAGGACATGT	GTCTGTGCAA	GCTGAATTTGA
901	AGCAAGTTAT	AGAGGTTTAT	GATTTGGTGA	GAGAAATGGG	TCCTGATCTG	GGGCTTTTAC	ATCTAAGACA	AGTCCAAAG	GCAGGACTGT	TATCTTTGGC
1001	CAATTGCCCC	GATTTTGCTA	GTGTTGTCT	TGGTAATGCT	TCAGGTCTAG	GTATAATCGG	AATGTACAGA	GGAAGAGTGC	CAACACAGAG	GCTATTTTCT
1101	GCAGCAGAAA	GTTATGCCAG	AAGCTTAAAA	GAAAGCAACA	AAATCAACTT	CTCCTCATTA	GGGCTCACAG	ACGAAGAAA	AGAAGCTGCA	GAACACTTCT
1201	TAAACATGAG	TGATGACAA	CAAGATGATT	ATGAGTAATT	AAAAAATGG	GACAAGTCAA	AATGTCAATC	CCTGAAGGAA	AAGATATCCT	GTTCATGGGT
1301	AATGAGCAG	CAAAATAGC	AGAACTTTC	CAGAAATCAC	TAAAAGATC	AGGTCAACAA	AGAACCCAGT	CTATTGTAGG	GGAAAAGTA	AACACTATAT
1401	CAGAAACTCT	AGAGCTACCT	ACCATCAGCA	AACCTGCACG	ATCATCTACA	CTGCTAGAGC	CAAAATTTGGC	ATGGCAGAC	AGCAGCAGAG	CCACCAAAAC
1501	CACAGAAAA	CAACCAACCA	AAACAACAGA	TCCTGTTGAA	GAAGAGGAAC	TCAATGAAAA	GAAGATATCA	CCTTCCAGTG	ATGGGAAGAC	TCCCGCAGAG
1601	AAAAATCAA	AATCTCAAC	CAATGTAATA	AAGAAAGTTT	CCTTCACATC	AAATGAAACCA	GGGAAATATA	CCAACTAGA	AAAAGATGCC	CTAGATTTCG
1701	TCAGAGATA	AATCAAGGAG	AAGATATTTA	CCAGTTAATC	ATGTAGTTTA	GAGTAGACCA	CATCTCACT	AGCATTTGAG	TCAGAGATGC	AATCAATAGA
1801	CTTATCAAGG	CATTCCTAC	ACAGCTGCTG	TTCAAGTTGA	TCTGGTAGAA	AAAGACTTAC	TACCAGCAAG	TTTGACAATA	TGGTTTCCTC	TATTTCCAGC
2301	CAACACACCA	CCAGCGGTTT	TGCTCGATCA	GCTAAAGACC	TTGACAATAA	CAACTCTGTA	TGCTGCATCA	CAGAAATGGT	CAATACTCAA	GGTAAATGCA
2401	TCAGTCAGG	GTGCTGCTAT	GTCTGTACTT	CCCAAAAAAT	TCGAAGTAAA	TGCAACTGTG	GCACTTGATG	AATACAGCAA	ACTTGACTTT	GACAAAGTTAA
2501	CGGTTTGGGA	TGTTAAACAA	GTTTATTTGA	CAACCATGAA	ACCATATGGG	ATGGTGTCAA	AATTTGTGAG	TTCAAGCCAA	TCAGTTGGCA	ACAAGACACA
2601	TGATCTAATT	GCACTGTGTG	ACTTCATGGA	CCTAGAGAAA	AATATACCTG	TGACATATCC	AGCATTCATA	AAGTCAGTTT	CAATCAAGA	GAGTGAGTCA
2701	GCCACTGTTG	AAGCTGCAAT	AAGCAGTGAG	GCCGACCAAG	CATTAAACACA	AGCCAAAATT	GCACCTTATG	CAGGACTAAT	CATGATCATG	ACCATGAACA
2801	ATCCAAAAGG	TATATTCAAG	AAACTAGGAG	CTGGAACACA	AGTGATAGTA	GAGCTAGGGG	CATATGTTCA	AGCCGAGAGC	ATCAGCAGGA	TCTGCAAGAG
2901	CTGGAGTCAC	CAAGGAACAA	GATATGTACT	AAATCCAGA	TAAAATAAAC	TGTCCTAATC	AATAATTGCT	TATATAATCT	TAAAGATCAA	TGAGCTTAT
3001	ATTATAGTTA	TATAAAAAA	TTTAGAACTA	GGAAGGTATT	AATAGAAAGC	GGGACAAGTA	AAAATGTCTT	GGAAAGTGAT	GATTATCAT	TCGTTACTCA
3101	TAAACCTTCA	GCACGGACTA	AAGGAAAGTT	ATTTAGAAGA	ATCATGTAGT	ACTATAACTG	AAGGATATCT	CAGTGTTTTA	AGAACAGGTT	GGTACACCAA
3201	TGCTTTTACA	TTAGAAGTTG	GTGATGTTGA	AAATCTTACA	TGTACTGATG	GACCTAGCTT	AATCAAAAACA	GAACCTGACC	TAAACAAAAG	TGCTCTAAGA
3301	GAATCTCAAA	CAGTTTCTGC	TGATCAGTTA	CGAGAGAGAA	AACAATTTGA	AAATCCAGAG	AATCAAGGT	TTGTCTTAGG	TGCAATAGCT	CTTGGTGTG
3401	CCACAGCAGC	AGCAGTCACA	GCAGGCATTG	CGATAGCCAA	AACCATAAGG	CTTGAGAGTG	CAATGAATGC	AGTCAAAAGT	GCTCTCAAAA	CAACCAATGA
3501	GGCAGTATCC	ACACTAGGAA	ATGGAGTGG	AGTCCCTAGC	ACCGCAGTAA	GAGAGCTGAA	AGAAATTTG	AGCAAAAACC	TGACTAGTGC	AATTAACAG
3601	AACAAATGTG	ACATTGCTGA	TCTGAAGATG	GCTGTGAGCT	TCAGTCAATT	CAACAGAAGA	TTCTTAAATG	TTGTGCGGCA	GTTTTAGAG	AAATGAGGGA
3701	TACACACAGC	AATATCATTT	GACCTAATGA	CTGATGCTGA	GCTGGCCAGA	GCTGTATCAT	ACATGCCAAC	ATCTGCAGGA	CAGATAAAAC	TAATGTTAGA

Fig. 39A

HMPV strain 75 (continued)

3801 GAACCGTGCA ATGGTGAGGA GAAAAGGATT TGAATCTTTG ATAGGGGTCT
3901 GATACACCTT GTTGGATAAT CAAGGCAGCT CCTCTTTGTT CAGAAAAGA
4001 ATGCAGGATC CACTGTTTAC TACCCAAATA AAAAGAGCTG CGAAACAAGA
4101 ATCAAGAGAA TGCAACATCA ACATATCTAC AACCAACTAC CCATGCAAG
4201 GCTTTGGTGG CTTGTACAA AGGGGTTAGC TGTTCAATTG GCAGTAATCG
4301 AGGAGCGAGA CACTGTAACTA ATTGACAACA CTGTGTATCA ACTAAGCAAA
4401 CGATCCAATC AAGTTTCTCTG AGGATCAGTT CAATGTTGCG CTTGATCAAG
4501 ATTCTGAACA GTGCAGAAA AGGAAACACT GGCTTCATTA TTGTAATAAT
4601 TAATCAAAAA AACAGGAAA CCACAGGGG CACCTCCAGA TCGTAATGGT
4701 CAATCATCA TGTCTCGTAA AGCTCCATGC AAATCTGAAG TACGGGGCAA
4801 CTGATAGGTA TTTATTGTTA AGATCAAAAT ATCTCTTGAA TCAGCTTTTA
4901 AGAAGACAGG ACTCAAGACT TTGTTCTTGG TTCTACTAAT GTGGTTCAAG
5001 CTACATAACA TAATAAACA GCTACAAGAA ATAGAAGTAA GACAGGCCAG
5101 TATCTTATAT GGAGATGAGC AAAACTCCTG CATCCTGTAT TAATAACCTA
5201 TTTATCAGCA GGAATCTGTA ATGACTCTTC ATATGCTTTC CAAGACAGTG
5301 GGCAGATGAT ATGATATGGA CACACAAAAGA ATTTAAAAGAG ACACGTCTGT
5401 ATAGAAATAA TATATGTTAA AGTTACTTTA AGTTAGTAAA AAATAAATAG
5501 CTTCAAGAAAT ATGTAATCAA CTCAAAAAAA CTCAAAAAAA ACATCAGGT
5601 AGTAACAATC ACTGTCAACT ATACAAAAGT AGAAAAATAT TTGCAGGCAT
5701 TCAACAACAA TCAGACCCAT TCCTGATCTA AATGCAGTAC AGTACCTGAA
5801 GTTGAGAAAT ACACACGAAT CAATGCACAA ATATAAAAAT ATATAGTTTC
5901 AGTTCTATGC GACAAAAAGT CAAAAACCAT GACAGAAAAA CATAGGAAAG
6001 GAGAAAACTC AGTTTTCAC ATTTAAATCA GAACAAATCA TATCTAGATC
6101 TCACAACACC CTGCGGTCTAT ATGCAATAT CAATGGTCAA ACCACTGTG
6201 ACAAGTGGCC ATGGAAGCAA GAGTGGAGAA CAITCGGGCA ATAGACATGT
6301 GCTACACTGA TCCTTATGAG ATCAACAGCA CCAAGTATGG CACTCAACAC
6401 ACTGTGTCAA CATGCCGCG GTAGAACCAA GCAAGAAGAC CCCAATGACC
6501 GACCACAGAG GATTCAACAT CTCTAGCAGC AACCTAGAG GACCATCTAC
6601 GACGAGCACA CAACACTGCT GAGATCAACC AACAGACAGA CCACCCAAAC
6701 CTCGAACCCAC AAGCACAGCT GCAACCCAAA CACTCAACAC CACCACCAA
6801 TGCCACAACCT CAAAGCAGCG ATCAACCAAC CCAGGCAGCA GACCCAGCT
6901 ACATCTTCTC CAAGTAGTTA ACAAAAAAAC TATAAAATAA CCATGAAAAAC
7001 ATGAATGTTT TGAGCGTATA TACTAATGAA ATAGCATCTG TTTGTGCATC
7101 CAATAACAA TGGATCGGTT TTGTGAATCC ACTGTCAATG TCTATCTTCC
7201 CACTCATGCC TTTGAAAAGA CCTATCTTAA AAAAGATAA CACTGTAAA
7301 GATGACCCAA ATGAAGATAT CAGATTATAA AGTGGTTGAA CCAATTATA
7401 AAACAATTCT TAACAAGAAAT TAAAAACATP AGTCCCTTAA AATTAGTAT
7501 TTAATTTTAT AGATGTGGAG TTTATACCGG TTTGGGTGAG CAATTGGTTT
7601 AGTAATAAGA ACTGGTTCAA TTTTATGCAG ATCACTAGGC AAGTTAGTTT
7701 GTAAGTTTTT TCACATATAA CCAACTGTTA ACATGGAAAG ATGTGATGTT

Fig. 39B

HMPV strain 75 (continued)

7801 AAAATCAAGA AGGACTAGGA TTTAGAAGTA ATCTACAAGG TATGTTAACT
7901 AGGGTTCTCA CTAGTGAAG AGTTCGAAGG CTTTATTATG AGTGAATTC
8001 TTAATAGGGT TGACTGAACA ATTATCAATG TTGAAGCTA AAAACAGATC
8101 TAGTACTTAA ATTATTAGG GACACTTTGA AAAGTATAAA ATTATTAAAT
8201 TGGACACCTT ATGGTAGATG AGAGGGAAGC AATGATGCT GTTAAATTA
8301 GGAGCATTTA TACTAAGAA TATAAAGGG TTGTAGATA ATAATAAAG
8401 ATTTCAAAGC TAAAGTTAC CTTAGCCAACT TTGAGCTAAG TGTACAAGAT
8501 AAAAACCAAT CTTGAGATGG TATTAAATGA TAAAGCAATA TCTCCACCA
8601 AAAATCAAT ATTTAGAAGA GGTCTTCAAT GCAAGTGACA GTCAAGAAGC
8701 ACCTCAAAGC TTATGTAACT AAACAAGAGT ATCTAAATGA CAAAGACAC
8801 TGCAATGCAA CTTGGCAAAC AAAGACAAT ACAGATACTA CCGAGAAAC
8901 GGTGACTTGG ATCTCCAAAG AATTATGGAA ATGAATCAG AACTTCTCTC
9001 CCATAGTAAC AGACCTAAGT AAATTCATC AAGCCTTAG ATATGAACCC
9101 ATTTTGTGG TTACATCTTA TTGTTCCCAT GACCACAATG ATATGTGAT
9201 GAAGAGCAA GTGGGCTATA CAGATACCAT ATGGAGGGA TTGAAGGGTG
9301 CTGTTAAGAC TCGTTGTGAG ATGACCTCTC TATTAAACGG AGACAATCAA
9401 AAAAGAGAT TATAGCTTAG CAATTAAAT GCTTAAAGAG ATAAGAGATG
9501 AGAGTCTTC AATTATAAG TAAGGTGAT CAATCTGAGG GGGTCTGCA
9601 TACTAGATCA CATTAAACT ATGTCAGAT CAATAGGAG TCTGTGTCAA
9701 TTTCTGGCTG TATAACTTAT ACATGCATGA GTCAAAACAG CATCCGTAG
9801 AGATTTTGT AGCTGAAGAA AGAAAATGAT GTGTTGACC TATGGATGAA
9901 TTTACAGAAG GACTCCTGAT TTCTTGACTG AAGCAATCAG CCATGTGGAT
10001 CTTTAAAGCC TTATTATCTA TAGAAAAGAA TGAAGGTGCT ACATTAACAA
10101 ACAAGTGATA TAAATAGAAC AGCAGTTACT AGCATACTGA GTCTATCTCC
10201 AAGTAGGGAT CATTGCAGAC AACATAACAC CTGTTTATCC TCACGGATG
10301 TATGATATCA GGTACAAAGT CTATAACTAA CCTATTGCAG AGAACATCTG
10401 TTAGGGTTGT TATCTAGGAT ATTGTCACTA ATAAATTAATA GTATAGAAAT
10501 TGAGAGAAA ATCATGGAAC AATATGGAAT TAGTAGGAGT GACATCTCCA
10601 AGGAATAAT ATTGAAAAT TCAGTACTGA CAAGACCACA AGAGGTCAGA
10701 GTTCTGTGTT ATAACAGACA AATTCTTTCA AAACAACAAA AAGAGCAACT
10801 GAAGATTGCT CAATAAGATT TGCATAGGAA GTTTAGGTAT TAGCTATAAA
10901 GTTATCTGTT AGTAGCAGAC CCATGGAAT CCCAGCTTCT GTTCCAGCTT
11001 AGTGAGAGGT TCGGGAACGA AGACATTAACT CTAGTGTTC AAAATGCAAT
11101 GCCCAAAACA ATTAGCTTTA ATCCCCCAAT TAGAAGAGAT AGATATTATG
11201 AACCTCCGAT CAACACATCT TCAGTCTCTGA CAATATAGAC ATATTAAAC
11301 TTAATTAAGA GAGAAAACCTA TTTCCATGGA AATAATTTAA TTGAATCTTT
11401 TAGAAAACAA TATCTTTAGG AAGACTGGG GTGATGGGT CATATCAGAT
11501 TTTATGTAGT TGGGGATCCC AAGGGAAAAA TGTAAAAGAT GAAGATATAA
11601 ATGTTACGCA AGTCACTGTT TGAATCAAG GTCAAAAAA GAATATGTT
11701 GGTATTAGA GCAGTTAAGA GTAGTAGAAT TGCATGAAGT ACCCTGATT

Fig. 39C

HMPV strain 75 (continued)

11801	GCAGTTAATA	GAACAAAGTC	TATCTTTAAG	AATAACTGTT	TTGAATTATA	CAGACATGGC	ACATGCTCTT	ACAGGATTA	TTAGGAAGAA	ATTGATGTCT	11900
11901	GATATGCAC	TCTTTAATCC	AAGTTTCATCA	CCATGTTT	GTCTAACTCA	AGTTATTGAT	CCTACAACAC	AGTAGACTA	TTTTCTAAG	GTAATATTGG	12000
12001	AAAGGTTAAA	AAGTTATGAC	ACCAGTTTCCAG	ACTACAACAA	AGGGAAGTTA	ACAAGAAATT	ACATGACATT	ATTACCATGG	CAGCAGCTAA	ACAGGTATAA	12100
12101	TTTTGTCTTT	AGTTCAACAG	GATGTAAAT	CAGCTTGAAG	ACATGCATCG	GGAAATTGAT	AAAGGACTTA	AACCTAAGG	TTCTTTACTT	TATTTGAGAA	12200
12201	GGAGCAGGTA	ACTGGATGGC	AAGAACAGCA	TGTGAGTATC	CTGACATAAA	ATTTGTATAT	AGGAGTTTAA	AGGATGATCT	TGATCACCAT	TACCCATTAG	12300
12301	AATATCAAAG	GGTAATAGGT	GATTTAAATA	GAGTAATAGA	TGGTGGTGAA	GGATTATCAA	TGGAGACCA	AGATGCAACT	CAAAAGACTC	ATTGGGACTT	12400
12401	GATACACAGA	ATAAGTAAAG	ATGCTTTTAT	GATAACATTG	TGTGATGCAG	AATTCAAAA	CAGAGATGAT	TTCTTTAAAA	TGGTAATCT	TTGGAGAAAA	12500
12501	CATGTATTAT	CATGTAGAAT	CTGTACAGCT	TATGGAACAG	ATCTTTACTT	ATTTGCAAG	TATCATGCGA	CGGACTGCAA	TATAAAGTTA	CCATTTTTTG	12600
12601	TAAGTCTGT	AGCTACTTTT	ATTATGCAAG	AGCAGTGTGT	GTCAGGATCA	GAATGTTACA	TACTTTTAA	ATTAGGTGAT	CACAATAATC	TGCCATGTCA	12700
12701	CGGAGAAATA	CAAAATTTCC	AAATGAGAA	AGCAATGAGT	AATGATTTCC	ATGCCCTAAA	AAACTAGAC	AACAAATCAA	TTGAAGCAAA	CTGCAATCT	12800
12801	CTTCTATCAG	GATTATAGAA	TCCAAATGGT	TAAAGAAAT	AGCAAGTACA	AAAGAACTG	TTAAACACTAC	AAAGCAATCA	TTCTTTCCATA	GCAACAGTTG	12900
12901	GCGGAAGTAA	GATTATAGAA	TCCAAATGGT	TAAAGAAAT	AGCAAGTACA	ATAATTTGAT	GTTAGAGCA	TATCTTGAAT	TCTCCAAGAG	GTGAATTTAA	13000
13001	CTATGATTTT	TTTGAAGCAT	TAGAGAACAC	ATATCCCAAT	ATGATCAAGC	TTATAGATAA	CCTGGGAAT	GCAGAGATAA	AAAAACTAAT	CAAAAGTTACC	13100
13101	GGGTATATGC	TTGTGAGTGA	GAAGTAAATA	TAAATAAAT	AATCAACCAT	AATCTCACAC	AATGAGAAA	ATGATCATCT	AACAGTTTAA	TTGACCATTA	13200
13201	GTAAATTAAA	AATTATAAAT	TAGTAACATA	TTGATAAAAA	ATAAGAAATT	GAAATTGAAT	GTATACGGTT	TTTTTGCCGT			13280

Fig. 39D